? b 155
14may03 11:19:38 User208669 Session D2288.1
$0.28 0.081 DialUnits File1
$0.28 Estimated cost File1
$0.28 Estimated cost this search
$0.28 Estimated total session cost 0.081 DialUnits
File 155:MEDLINE(R) 1966-2003/May W1
(c) format only 2003 The Dialog Corp.
*File 155: Medline has been reloaded and accession numbers have changed. Please see HELP NEWS 155.
Set Items Description
--- ----- -----------
? ds
Set Items Description
S1 19809 VIRUS AND (RECEPTOR OR RECEPTORS)
S2 930316 DT=REVIEW?
S3 2087 S1 AND S2
S4 11103 S1/TI
S5 702 S4 AND S3
S6 142 SEQUENC? AND S5
S7 25362 CAR OR HCAR OR MCAR OR COXSACKIE OR ADENOVIRUS
S8 65 S3 AND S7
S9 0 VIRAL ADJ RECEPTOR?
S10 1384 VIRAL (W) RECEPTOR?
S11 160 S2 AND S10
S12 35 S10/TI
S13 294214 MUTATION OR MUTANT
S14 593482 RECEPTOR OR RECEPTORS
S15 9325 S13 (3N)S14
S16 463 S1 AND S15
S17 24 S2 AND S16
S18 4860 S13 (N)S14
S19 232 S18 AND S1
? t s6/7/13
6/7/13
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
11640582 99074492 PMID: 9852300
CD46 (membrane cofactor protein of complement, measles virus receptor): structural and functional divergence among species (review).
Seya T; Nomura M; Murakami Y; Begum N A; Matsumoto M; Nagasawa S
Department of Immunology, Osaka Medical Center for Cancer and Cardiovascular Diseases, Higashinari-ku, Osaka 537, Japan.
International journal of molecular medicine (GREECE) May 1998, 1 (5) p809-16, ISSN 1107-3756 Journal Code: 9810955
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Human CD46 was identified as a complement regulator and was later shown to be a measles virus receptor. The ubiquitous distribution profile of CD46 accounted for systemic measles infection and general protection of host tissue/organs from autologous complement. A similar ubiquitous distribution was observed for swine and simian CD46 homologues based upon subsequent cDNA cloning and Northern analysis, reinforcing the roles of CD46. In contrast, recent cDNA cloning and distribution analyses of murine and guinea-pig CD46 revealed the predominant expression of these rodent CD46 homologues in the testis, especially in mature testicular germ cells. These results do not support the established functions of human CD46 but support the hypothesis that CD46 on sperm serves as a fertilization-related adhesion molecule toward eggs. Here, we review the structure, function and distribution of human CD46 and discuss the possible differences between human CD46 and its homologues recently cloned from a variety of non-human primates and other animals. (72 Refs.)
Record Date Created: 19990224
Record Date Completed: 19990224
? t s8/7/2 20 26 47 53 54
8/7/2
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
14742747 22514653 PMID: 12627395
Structural evidence for common functions and ancestry of the reovirus and adenovirus attachment proteins.
Stehle Thilo; Dermody Terence S
Laboratory of Developmental Immunology and Renal Unit, Massachusetts General Hospital, Harvard Medical School, Boston, MA 02114, USA. tstehle@partners.org
Reviews in medical virology (England) Mar-Apr 2003, 13 (2) p123-32, ISSN 1052-9276 Journal Code: 9112448
Contract/Grant No.: AI38296; AI; NIAID; AI45716; AI; NIAID
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
The crystal structure of the reovirus attachment protein, sigma1, reveals a fibre-like structure that is remarkably similar to that of the adenovirus attachment protein, fibre. Both proteins are trimers with head-and-tail morphology. They share unique domain structures and functional properties including defined regions of flexibility within the tail and an unusual symmetry mismatch with the pentameric viral capsid protein into which they are inserted. Moreover, the receptors for reoviruses and adenoviruses, junctional adhesion molecule 1 and coxsackievirus and adenovirus receptor, respectively, also share key structural and functional properties. Although reoviruses and adenoviruses belong to different virus families and have few

properties in common, the observed similarities between sigma1 and fibre point to a conserved mechanism of attachment and an ancient evolutionary relationship. Copyright 2003 John Wiley & Sons, Ltd. (66 Refs.)
Record Date Created: 20030310
Record Date Completed: 20030425

8/7/20
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
11427447 98309961 PMID: 9645993
Coxsackie B virus and its interaction with permissive host cells.
Selinka H C; Huber M; Pasch A; Klingel K; Aepinus C; Kandolf R
Department of Molecular Pathology, University of Tubingen, Germany. hans-christoph.selinka@med.uni-tuebingen.de
Clinical and diagnostic virology (NETHERLANDS) Apr 1998, 9 (2-3) p115-23, ISSN 0928-0197 Journal Code: 9309653
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
BACKGROUND: Observations in humans and the results of experiments on laboratory animals have provided evidence that coxsackieviruses of group B (CVB) are major etiologic agents of acute and chronic enterovirus myocarditis and various other virus-induced diseases. OBJECTIVE: This minireview briefly summarizes the investigations to elucidate various molecular mechanisms for the induction and maintenance of persistent CVB infections. With regard to the recent findings that CVB may use several different receptor proteins, this article focuses on virus-host cell interactions and the potential impact of these interactions for enteroviral replication. STUDY DESIGN: The interaction of CVB with specific cell surface proteins was analyzed in cultured cell lines and murine tissues at the level of virus attachment and virus internalization. As example for the interaction of CVB with intracellular proteins, the state of p21rasGTPase-activating protein (RasGAP) was investigated in mock-infected and CVB3-infected HeLa cells. RESULTS AND CONCLUSIONS: The experiments to elucidate the virus receptor interactions revealed the necessity to differentiate between CVB attachment proteins and proteins involved in virus internalization. Since more than one protein may be required to initiate the uptake of CVB into permissive host cells, a model of the putative interaction of these proteins within a multimeric receptor complex is proposed. It is further tempting to speculate that the presence of multiple attachment proteins may influence the tissue tropism of CVB as well as pathogenicity. (39 Refs.)
Record Date Created: 19980916
Record Date Completed: 19980916

8/7/26
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
11085523 97440728 PMID: 9294931
Identification and biology of cellular receptors for the coxsackie B viruses group.
Kuhn R J
Department of Biological Sciences, Purdue University, West Lafayette, Indiana 47907, USA.
Current topics in microbiology and immunology (GERMANY) 1997, 223 p209-26, ISSN 0070-217X Journal Code: 0110513
Document type: Journal Article; Review; Review Literature
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
(65 Refs.)
Record Date Created: 19971022
Record Date Completed: 19971022

8/7/47
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
09588865 21372597 PMID: 11479928
Receptor for the group B coxsackieviruses and adenoviruses: CAR.
Carson S D
Department of Pathology and Microbiology, University of Nebraska Medical Center, Omaha, NE 68198-6495, USA. scarson@unmc.edu
Reviews in medical virology (England) Jul-Aug 2001, 11 (4) p219-26, ISSN 1052-9276 Journal Code: 9112448
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Considerable progress towards the characterisation of the long-sought receptor, CAR (coxsackievirus and adenovirus receptor), shared by group B coxsackieviruses (CVB) and most adenoviruses (Ad) has been made since it was isolated and cloned in 1997. The primary sequence of CAR shows that it is a member of the immunoglobulin superfamily of proteins, containing two Ig superfamily domains: an amino-terminal V-like module and a C2-like module. The CAR cytoplasmic domain, representing nearly one-third of the protein, is separated from the C2-like module by a single membrane-spanning sequence. The structure of the CAR V-like module complexed with the Ad fibre knob has been determined using recombinant proteins, and reveals three CAR modules associated with a single knob. Although recombinant CAR expressed in mammalian cells confers permissivity to CVB infection, details of the interaction between CAR and CVB remain to be elucidated. The expression of CAR appears to be highly regulated with respect to both cell type and developmental age. In rodents, CAR is expressed at high levels

just before birth, and declines thereafter. Expressed levels have been found to increase in regenerating muscle and in response to immunological mediators or inflammation, and in RD cells and umbilical vein endothelial cells in response to high cell density. These studies indicate that CAR expression is highly regulated, but the mechanisms and molecules that mediate the expression remain to be discovered. The physiological function of CAR and its natural ligand also remain to be discovered. In addition, while CAR expression generally correlates with viral tropism, the relationship between the physiological function of CAR and the pathologies of CVB and Ad infections remain to be described. Copyright 2001 John Wiley & Sons, Ltd. (45 Refs.)
Record Date Created: 20010731
Record Date Completed: 20020404

8/7/53
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
09098690 20396567 PMID: 10936081
Cell receptors involved in adenovirus entry.
Nemerow G R
Department of Immunology, Scripps Research Institute, La Jolla, California 92037, USA. gnemerow@scripps.edu
Virology (UNITED STATES) Aug 15 2000, 274 (1) p1-4, ISSN 0042-6822 Journal Code: 0110674
Contract/Grant No.: EY11431; EY; NEI; HL54352; HL; NHLBI
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
(18 Refs.)
Record Date Created: 20000925
Record Date Completed: 20000925

8/7/54
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
09016780 20310108 PMID: 10851559
[Cell receptors for human adenoviruses]
Recepteurs cellulaires des adenovirus humains.
Boulanger P
Laboratoire de Virologie et Pathogenese Moleculaire, Faculte de Medecine de Montpellier, CNRS UMR 5812, Montpellier.
Journal de la Societe de biologie (FRANCE) 1999, 193 (1) p77-84, Journal Code: 100890617
Document type: Journal Article; Review; Review, Tutorial ; English Abstract
Languages: FRENCH
Main Citation Owner: NLM
Record type: Completed
During the early stage of the adenovirus infection, the virion binds to a "primary receptor" on the host cell plasma membrane via the fibre projection jetting out of the penton base capsomers located at the twelve apices of the icosahedral capsid. The second step consists of a receptor-mediated endocytosis which involves membrane integrin molecules (the "secondary receptors") and the RGD and/or LDV motifs of penton base. The latter step is inhibited at low temperature, whereas virus attachment to its primary receptor is temperature-independent. Two different primary receptors with a high affinity for the Adenovirus have been recently identified. One is common to Coxsackievirus B3 and adenovirus (CAR), the other one corresponds to a conserved region of the alpha-2 domain of the heavy chain of the major histocompatibility complex class I molecules (MHC-I-alpha 2), overlapping tryptophane-167. The receptor usage by the virus is governed by both cellular and viral parameters. On the cellular side, the relative abundance of one versus the other type of primary receptors would theoretically determine the virus choice: CAR receptor has been mainly found in tissues from mesodermic origin, whereas MHC-I-alpha 2 is ubiquitous. On the virus side, the molecular determinants of the receptor usage have been mapped to the terminal knob of the fiber projection, and have been found to be different for CAR and MHC-I-alpha 2. CAR recognizes linear motifs in fiber knobs in a subgroup-dependent manner, as it binds to all Adenovirus serotypes except for the subgroup B members. MHC-I-alpha 2 however recognizes conformational epitopes carried by fiber knobs from all serotypes tested including subgroup B members. These results should have significant implications in the cell targeting of adenoviral vectors used in gene therapy. (56 Refs.)
Record Date Created: 20000630
Record Date Completed: 20000630
? t s12/7/21 22
12/7/21
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
07367084 92230251 PMID: 1566586
A single point mutation of the influenza C virus glycoprotein (HEF) changes the viral receptor-binding activity.
Szepanski S; Gross H J; Brossmer R; Klenk H D; Herrler G
Institut fur Virologie, Philipps-Universitat Marburg, Germany.
Virology (UNITED STATES) May 1992, 188 (1) p85-92, ISSN 0042-6822 Journal Code: 0110674
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
From strain JHB/1/66 of influenza C virus a mutant was derived with a change in the cell tropism. The mutant was able to grow in a subline of

Madin-Darby canine kidney cells (MDCK II) which is resistant to infection by the parent virus due to a lack of receptors. Inactivation of cellular receptors by either neuraminidase or acetylesterase and generation of receptors by resialylation of cells with N-acetyl-9-O-acetylneuraminic acid (Neu5,9Ac2) indicated that 9-O-acetylated sialic acid is a receptor determinant for both parent and mutant virus. However, the mutant required less Neu5,9Ac2 on the cell surface for virus attachment than the parent virus. The increased binding efficiency enabled the mutant to infect cells with a low content of 9-O-acetylated sialic acid which were resistant to the parent virus. By comparing the nucleotide sequences of the glycoprotein (HEF) genes of the parent and the mutant virus only a single point mutation could be identified on the mutant gene. This mutation at nucleotide position 872 causes an amino acid exchange from threonine to isoleucine at position 284 on the amino acid sequence. Sequence similarity with a stretch of amino acids involved in the receptor-binding pocket of the influenza A hemagglutinin suggests that the mutation site on the influenza C glycoprotein (HEF) is part of the receptor-binding site.
Record Date Created: 19920515
Record Date Completed: 19920515

12/7/22
DIALOG(R)File 155:MEDLINE(R)

06152964 89168410 PMID: 2538240
Viral receptors of the immunoglobulin superfamily.
White J M; Littman D R
Department of Pharmacology, University of California, San Francisco 94143.
Cell (UNITED STATES) Mar 10 1989, 56 (5) p725-8, ISSN 0092-8674 Journal Code: 0413066
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
(18 Refs.)
Record Date Created: 19890425
Record Date Completed: 19890425
? t s19/7/5
19/7/5
DIALOG(R)File 155:MEDLINE(R)

14198605 22326847 PMID: 12438620
Mutations in the N-terminal domains of nectin-1 and nectin-2 reveal differences in requirements for entry of various alphaherpesviruses and for nectin-nectin interactions.
Struyf Frank; Martinez Wanda M; Spear Patricia G; et al
Department of Microbiology-Immunology, The Feinberg School of Medicine, Northwestern University, 320 E. Superior Street, Chicago, IL 60611, USA.
Journal of virology (United States) Dec 2002, 76 (24) p12940-50, ISSN 0022-538X Journal Code: 0113724
Contract/Grant No.: F32 GM 19765; GM; NIGMS; R01 AI 49394; AI; NIAID; R37 AI 36293; AI; NIAID; +
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Nectin-1 and nectin-2 are related molecules that can function with different specificities as entry receptors for mammalian alphaherpesviruses through interaction with viral glycoprotein D (gD). The normal function of members of the nectin family is to mediate cell-cell adhesion through homotypic and heterotypic nectin-nectin interactions in cadherin-based adherens junctions. We examined mutations in three equivalent regions of the N-terminal V-like domains of nectin-1 and nectin-2 to test the effects on entry of various alphaherpesviruses, nectin-nectin interactions, and interactions of the mutant nectins with gD. Mutations in region I previously shown to severely impair herpes simplex virus (HSV) entry activity, but not pseudorabies virus (PRV) or bovine herpesvirus 1 (BHV-1) entry, did not reduce homotypic trans interactions for either nectin-1 or nectin-2 or binding of nectin-3 to nectin-1. Mutations in region II, patterned after a reported single-nucleotide polymorphism in nectin-2, enhanced intracellular accumulation of both nectin-1 and nectin-2 and had a deleterious effect on all of the activities under study. Mutations in region III previously shown to reduce homotypic trans interactions of nectin-2 impaired the entry of PRV and BHV-1 when introduced into either nectin-1 or nectin-2, but only the nectin-2 mutation reduced HSV entry activity. Binding of nectin-1 to nectin-3 was not affected. Effects of the nectin-1 and nectin-2 mutations on interactions with gD did not necessarily correlate with entry activity of the mutant receptors. We can conclude that structural requirements for HSV entry, PRV and BHV-1 entry, and homotypic and heterotypic trans interactions are all different despite the previously reported ability of HSV and HSV gD to inhibit trans interactions.
Record Date Created: 20021119
Record Date Completed: 20021219
? log hold
14may03 11:45:53 User208669 Session D2288.2
$12.26 3.832 DialUnits File155
$0.00 154 Type(s) in Format 6
$2.31 11 Type(s) in Format 7
$2.31 165 Types
$14.57 Estimated cost File155
$6.30 TELNET
$20.87 Estimated cost this search
$21.15 Estimated total session cost 3.913 DialUnits
Logoff: level 02.14.01 D 11:45:54

? b 155,357
28aug02 09:50:03 User208669 Session D2092.2
$0.12 0.037 DialUnits File155
$0.12 Estimated cost File155
$0.30 0.037 DialUnits File359
$0.30 Estimated cost File359
OneSearch, 2 files, 0.074 DialUnits FileOS
$0.01 TELNET
$0.43 Estimated cost this search
$0.78 Estimated total session cost 0.172 DialUnits

SYSTEM:OS - DIALOG OneSearch
File 155:MEDLINE(R) 1966-2002/Aug W4
*File 155: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.
File 357:Derwent Biotech Res. 1982-2002/June W1
(c) 2002 Thomson Derwent & ISI
*File 357: File enhancements now online. See HELP NEWS 357. Alert feature enhanced for multiple files, etc. See HELP ALERT.

Set Items Description
--- ----- -----------
? ds
Set Items Description
S1 206 COXSACKIE AND RECEPTOR
S2 220222 TERMINUS OR TERMINAL
S3 9 S1 AND S2
S4 156542 DOMAIN OR DOMAINS
S5 38 S1 AND S4
S6 29 RD (unique items)
? t s3/7/2
3/7/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
11290763 21326079 PMID: 11316797
Multiple regions within the coxsackievirus and adenovirus receptor cytoplasmic domain are required for basolateral sorting.
Cohen C J; Gaetz J; Ohman T; Bergelson J M
Division of Immunologic and Infectious Diseases, The Children's Hospital of Philadelphia, Philadelphia, PA 19104-4318, USA. cohenc@email.chop.edu
Journal of biological chemistry (United States) Jul 6 2001, 276 (27) p25392-8, ISSN 0021-9258 Journal Code: 2985121R
Contract/Grant No.: HL54734; HL; NHLBI; T32 AI07278; AI; NIAID
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
The coxsackievirus and adenovirus receptor (CAR) mediates attachment and infection by coxsackie B viruses and many adenoviruses. In human airway epithelia, as well as in transfected Madin-Darby canine kidney cells, CAR is expressed exclusively on the basolateral surface. Variants of CAR that lack the cytoplasmic domain or are attached to the cell membrane by a glycosylphosphatidylinositol anchor are expressed on both the apical and basolateral surfaces. We have examined the localization of CAR variants with progressive truncations of the cytoplasmic domain, as well as with mutations that ablate a potential PDZ (PSD95/dlg/ZO-1) interaction motif and a putative tyrosine-based sorting signal. In addition, we have examined the targeting of two murine CAR isoforms, with different C-terminal sequences. The results suggest that multiple regions within the CAR cytoplasmic domain contain information that is necessary for basolateral targeting.
Record Date Created: 20010702
? t s6/7/7 15 17 22 27
6/7/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
12604321 21547769 PMID: 11688979
Characterization of a cDNA encoding the bovine coxsackie and adenovirus receptor.
Thoelen I; Keyaerts E; Lindberg M; Van Ranst M
Laboratory of Clinical and Epidemiological Virology, University of Leuven, Belgium.
Biochemical and biophysical research communications (United States) Nov 9 2001, 288 (4) p805-8, ISSN 0006-291X Journal Code: 0372516
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Non-human adenoviruses such as bovine adenovirus type 3 (BAV-3) that do not replicate in human cells but can infect human cells in culture could provide an attractive alternative to human adenoviral vectors for gene therapy. In addition, a large-animal model for genetic diseases can be very useful for the assessment of the efficacy of adenovector-mediated gene delivery in man. Recombinant human subgroup C adenovectors use the coxsackie and adenovirus receptor (CAR) to enter their target cells. Through RT-PCR and sequencing we determined the complete coding sequence of bovine CAR which serves as the primary adenoviral attachment site on bovine cells. A multiple sequence alignment, involving all the previously identified CAR species (man, mouse, rat, pig, and dog) showed that bovine CAR was most related to porcine CAR (92% nucleotide similarity) and demonstrated a highly conserved adenovirus binding Ig1 domain. Copyright 2001 Academic Press.
Record Date Created: 20011105

6/7/15 (Item 15 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

11071013 21093138 PMID: 11177539
Manipulation of the cytoplasmic and transmembrane domains alters cell surface levels of the coxsackie-adenovirus receptor and changes the efficiency of adenovirus infection.
van't Hof W; Crystal R G
Division of Pulmonary and Critical Care Medicine, Weill Medical College of Cornell University, New York, NY 10021, USA.
Human gene therapy (United States) Jan 1 2001, 12 (1) p25-34, ISSN 1043-0342 Journal Code: 9008950
Contract/Grant No.: HL51746-06A1; HL; NHLBI
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Expression of the coxsackie-adenovirus receptor (CAR) is a critical determinant in cellular susceptibility to infection with adenovirus-based gene transfer vectors. This study is focused on the hypothesis that manipulation of the cytoplasmic tail and transmembrane regions of CAR can be used to change cell surface levels of CAR and, consequently, to alter the efficiency of Ad-mediated gene transfer. To accomplish this, Flag-tagged ([F]) human CAR ([F]CAR), [F]tailless-CAR (lacking the cytoplasmic tail), and [F]GPI-CAR (containing a GPI lipid anchor instead of the transmembrane and cytoplasmic regions) were exogenously expressed in CHO cells. Analysis of (125)I-labeled anti-Flag antibody binding to transfected cells revealed that [F]tailless-CAR and [F]GPI-CAR were expressed on the cell surface in 1.8- to 2.5-fold higher amounts than [F]CAR, while the total expression levels were similar. Infection with replication-deficient adenovirus encoding beta-galactosidase (Ad-betagal) demonstrated 1.5- to 2-fold higher levels of transgene expression in CHO cells expressing [F]tailless-CAR or [F]GPI-CAR, respectively, compared with cells containing [F]CAR. The form of CAR expressed did not affect the transport of fluorescent Cy3-Ad particles from the cell surface to the nuclear region. These observations indicate that transduction of target cells by Ad vectors can be optimized by increasing cell surface levels of CAR through functional deletion of the tail and membrane protein domains.
Record Date Created: 20010222

6/7/17 (Item 17 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
10511152 20036898 PMID: 10567268
Structural analysis of the mechanism of adenovirus binding to its human cellular receptor, CAR.
Bewley M C; Springer K; Zhang Y B; Freimuth P; Flanagan J M
Biology Department, Brookhaven National Laboratory, Upton, NY 11973, USA.
Science (UNITED STATES) Nov 19 1999, 286 (5444) p1579-83, ISSN 0036-8075 Journal Code: 0404511
Contract/Grant No.: 1P41 RR12408-01A1; RR; NCRR
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Binding of virus particles to specific host cell surface receptors is known to be an obligatory step in infection even though the molecular basis for these interactions is not well characterized. The crystal structure of the adenovirus fiber knob domain in complex with domain I of its human cellular receptor, coxsackie and adenovirus receptor (CAR), is presented here. Surface-exposed loops on knob contact one face of CAR, forming a high-affinity complex. Topology mismatches between interacting surfaces create interfacial solvent-filled cavities and channels that may be targets for antiviral drug therapy. The structure identifies key determinants of binding specificity, which may suggest ways to modify the tropism of adenovirus-based gene therapy vectors.
Record Date Created: 19991209

6/7/22 (Item 22 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
10092971 99077161 PMID: 9862345
CTX, a Xenopus thymocyte receptor, defines a molecular family conserved throughout vertebrates.
Chretien I; Marcuz A; Courtet M; Katevuo K; Vainio O; Heath J K; White S J; Du Pasquier L
Basel Institute for Immunology, Switzerland.
European journal of immunology (GERMANY) Dec 1998, 28 (12) p4094-104 , ISSN 0014-2980 Journal Code: 1273201
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
CTX, a cortical thymocyte marker in Xenopus, is an immunoglobulin superfamily (Igsf) member comprising one variable and one constant C2-type Igsf domain, a transmembrane segment and a cytoplasmic tail. Although resembling that of the TCR and immunoglobulins, the variable domain is not encoded by somatic rearrangement of the gene but by splicing of two half-domain exons. The C2 domain, also encoded by two exons, has an extra pair of cysteines. The transmembrane segment is free of charged residues, and the cytoplasmic tail (70 amino acids) contains one tyrosine and many glutamic acid residues. ChT1, a chicken homologue of CTX, has the same structural and genetic features, and both molecules are expressed on the thymocyte surface. We cloned new mouse (CTM) and human (CTH) cDNA and genes which are highly homologous to CTX/ChT1 but not lymphocyte specific. Similarity with recently described human cell surface molecules, A33 antigen and CAR (coxsackie and adenovirus 5 receptor), and a number of expressed sequence tags leads us to propose that CTX defines a novel subset of the Igsf, conserved throughout vertebrates and extending beyond the

immune system. Strong homologies within vertebrate sequences suggest that the V and C2 CTX domains are scions of a very ancient lineage.
Record Date Created: 19990105

6/7/27 (Item 5 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
(c) 2002 Thomson Derwent & ISI. All rts. reserv.
0256200 DBA Accession No.: 2000-10690
Ectodomain of coxsackie virus and adeno virus receptor genetically fused to epidermal growth factor mediates adeno virus targeting to epidermal growth factor receptor-positive cells - human adeno virus vector cell targeting improvement by epidermal growth factor and coxsackie virus and adeno virus receptor fusion protein for improved gene therapy
AUTHOR: Dmitriev I; Kashentseva E; Rogers B E; Krasnykh V; +Curiel D T
CORPORATE AFFILIATE: Univ.Alabama
CORPORATE SOURCE: Division of Human Gene Therapy, Dept. of Medicine, Pathology and Surgery, Gene Therapy Center, University of Alabama at Birmingham, 1824 6th Ave., South Room WTI 620, Birmingham, AL 35294-3300, USA. email:david.curiel@ccc.uab.edu
JOURNAL: J.Virol. (74, 15, 6875-84) 2000
ISSN: 0022-538X CODEN: JOVIAM
LANGUAGE: English
ABSTRACT: Use of adeno virus (AV) vectors for gene therapy is limited by low efficiency of AV-mediated gene transfer to target cells expressing marginal levels of AV fiber receptor. AV vectors could be improved by modifying AV tropism to target the virus to specific organs/tissues. The fact that the coxsackie virus and AV receptor (CAR) does not play a role in virus internalization, but acts as the virus attachment site, suggests that the extracellular part of CAR may be used to block the receptor recognition site of the AV fiber knob domain. Bispecific fusion proteins may be designed by a recombinant soluble form of truncated CAR (sCAR) and a targeting ligand. sCAR was genetically fused with human epidermal growth factor (EGF) and studied with respect to its ability to target AV infection to the EGF receptor overexpressed on cancer cell lines. sCAR-EGF protein bound to AV virions and directed them to EGF receptor, thereby achieving targeted delivery of reporter gene. sCAE-EGF protein is able to retarget AV via a non-CAR pathway, with attachment of gene transfer efficiency. (55 ref)
? log hold
28aug02 09:58:35 User208669 Session D2092.3
$2.82 0.881 DialUnits File155
$0.00 28 Type(s) in Format 6
$1.05 5 Type(s) in Format 7
$1.05 33 Types
$3.87 Estimated cost File155
$4.03 0.236 DialUnits File357
$0.00 10 Type(s) in Format 6
$2.70 1 Type(s) in Format 7
$2.70 11 Types
$6.73 Estimated cost File357
OneSearch, 2 files, 1.117 DialUnits FileOS
$1.95 TELNET
$12.55 Estimated cost this search
$13.33 Estimated total session cost 1.289 DialUnits
Logoff: level 02.08.23 D 09:58:35

Reconnected in file OS 28aug02 10:28:19
*** ***

SYSTEM:OS - DIALOG OneSearch
File 155:MEDLINE(R) 1966-2002/Aug W4
*File 155: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.
File 357:Derwent Biotech Res. 1982-2002/June W1
(c) 2002 Thomson Derwent & ISI
*File 357: File enhancements now online. See HELP NEWS 357. Alert feature enhanced for multiple files, etc. See HELP ALERT.

Set Items Description
--- ----- -----------
? ds
Set Items Description
S1 206 COXSACKIE AND RECEPTOR
S2 220222 TERMINUS OR TERMINAL
S3 9 S1 AND S2
S4 156542 DOMAIN OR DOMAINS
S5 38 S1 AND S4
S6 29 RD (unique items)
S7 159047 CYTOPLASM?
S8 14 S1 AND S7
? log hold
28aug02 10:30:02 User208669 Session D2092.4
$0.90 0.282 DialUnits File155
$0.00 10 Type(s) in Format 6
$0.00 10 Types
$0.90 Estimated cost File155
$1.36 0.080 DialUnits File357
$0.00 4 Type(s) in Format 6
$0.00 4 Types
$1.36 Estimated cost File357
OneSearch, 2 files, 0.361 DialUnits FileOS
$0.43 TELNET
$2.69 Estimated cost this search
$2.69 Estimated total session cost 0.361 DialUnits

Logoff: level 02.08.23 D 10:30:02

? b 155,357
28aug02 11:02:35 User208669 Session D2093.1
$0.28 0.081 DialUnits File1
$0.28 Estimated cost File1
$0.01 TELNET
$0.29 Estimated cost this search
$0.29 Estimated total session cost 0.081 DialUnits

SYSTEM:OS - DIALOG OneSearch
File 155:MEDLINE(R) 1966-2002/Aug W4
*File 155: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.
File 357:Derwent Biotech Res. 1982-2002/June W1
(c) 2002 Thomson Derwent & ISI
*File 357: File enhancements now online. See HELP NEWS 357. Alert feature enhanced for multiple files, etc. See HELP ALERT.

Set Items Description
--- ----- -----
? s acvrp
S1 1 ACVRP
? t s1/7/1
1/7/1 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
(c) 2002 Thomson Derwent & ISI. All rts. reserv.
0242449 DBA Accession No.: 1999-13214 PATENT
Isolated and purified polynucleotide useful for treating or preventing cancer, inflammation and virus disorders - recombinant virus-receptor protein production via vector-mediated gene transfer and expression in host cell for diagnosis, prevention, therapy and gene therapy
AUTHOR: Lal P; Corley N C
CORPORATE SOURCE: Palo Alto, CA, USA.
PATENT ASSIGNEE: Incyte-Pharm. 1999
PATENT NUMBER: US 5942606 PATENT DATE: 19990824 WPI ACCESSION NO.:
1999-493538 (1941)
PRIORITY APPLIC. NO.: US 979424 APPLIC. DATE: 19971124
NATIONAL APPLIC. NO.: US 979424 APPLIC. DATE: 19971124
LANGUAGE: English
ABSTRACT: An isolated and purified polynucleotide (I) which encodes a protein with the virus-receptor protein (ACVRP) sequence of 390 amino acids (specified), is new. Also claimed are: a composition containing (I); an isolated and purified polynucleotide fully complementary to (I); an isolated and purified polynucleotide (III); an isolated and purified polynucleotide fully complementary to (III); an expression vector containing (I); a host cell transformed with the expression vector; and a method for detecting (I) in a biological sample containing nucleic acids, which consists of hybridizing the polynucleotide to the nucleic acids of the biological sample to form a hybridization complex and detecting the presence of the hybridization complex, therefore indicating the presence of the polynucleotide which encodes the protein in the sample. The administration of a vector which expressed a polynucleotide which is fully complementary to (I) may be useful for the prevention or treatment of cancer, a virus disorder or inflammation. The polynucleotides which encode ACVRP may be useful for diagnostic purposes and the expression vectors which encode ACVRP may be used for gene delivery. (28pp)
? b 155, 5
28aug02 11:03:18 User208669 Session D2093.2
$0.21 0.066 DialUnits File155
$0.21 Estimated cost File155
$3.97 0.233 DialUnits File357
$0.00 1 Type(s) in Format 6
$2.70 1 Type(s) in Format 7
$2.70 2 Types
$6.67 Estimated cost File357
OneSearch, 2 files, 0.299 DialUnits FileOS
$0.21 TELNET
$7.09 Estimated cost this search
$7.38 Estimated total session cost 0.380 DialUnits

SYSTEM:OS - DIALOG OneSearch
File 155:MEDLINE(R) 1966-2002/Aug W4
*File 155: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.
File 5:Biosis Previews(R) 1969-2002/Aug W4
(c) 2002 BIOSIS
*File 5: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

Set Items Description
--- ----- -----
? ds
Set Items Description
S1 412 AU=LAL P?
S2 236 AU=CORLEY N?
S3 113 S1 AND S2
S4 940879 RECEPTOR
S5 4 S3 AND S4
S6 10480 CAR OR (COXSACKIE AND RECEPTOR?)
S7 110 HCAR OR MCAR
S8 10542 S6 OR S7

S9 397164 HOMOLOG?
S10 186 S9 AND S8
S11 134 RD (unique items)
S12 60 S4 AND S11
? t s5/7/3
5/7/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2002 BIOSIS. All rts. reserv.
12195930 BIOSIS NO.: 199900490779
Viral receptor protein.
AUTHOR: Lal Preeti(a); Corley Neil C
AUTHOR ADDRESS: (a)VISX Inc., Santa Clara, CA**USA
JOURNAL: Official Gazette of the United States Patent and Trademark Office Patents 1225 (4):pNO PAGINATION Aug. 24, 1999
ISSN: 0098-1133
DOCUMENT TYPE: Patent
RECORD TYPE: Citation
LANGUAGE: English
? log hold
28aug02 11:07:46 User208669 Session D2093.3
$3.78 1.180 DialUnits File155
$0.00 61 Type(s) in Format 6
$0.00 61 Types
$3.78 Estimated cost File155
$4.88 0.871 DialUnits File5
$0.00 13 Type(s) in Format 6
$1.75 1 Type(s) in Format 7
$1.75 14 Types
$6.63 Estimated cost File5
OneSearch, 2 files, 2.051 DialUnits FileOS
$1.08 TELNET
$11.49 Estimated cost this search
$18.87 Estimated total session cost 2.431 DialUnits
Logoff: level 02.08.23 D 11:07:46

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 16:13:17 ; Search time 57.91 Seconds
(without alignments)
748.036 Million cell updates/sec

Title: US-09-902-759-39
Perfect score: 2012
Sequence: 1 MISLPGPLVTNLLRFLFLGL.....SRMGAVPVMVPAQSQAGSLV 390

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2012	100.0	390	20	AAY27096	Human viral recept
2	2012	100.0	390	20	AAY13351	Amino acid sequenc
3	2012	100.0	390	20	AAY05286	EGF-like homologue
4	2012	100.0	390	21	AAY88574	Human PRO246 amino
5	2012	100.0	390	21	AAY94999	Human secreted pro
6	2012	100.0	390	22	AAU12340	Human PRO246 polyp
7	2012	100.0	390	22	AAB88358	Human membrane or
8	2012	100.0	390	22	AAB68599	PRO246. Homo sapi
9	2012	100.0	390	22	AAB31207	Amino acid sequenc
10	2012	100.0	390	22	AAB80219	Human PRO246 prote
11	2012	100.0	390	22	AAB53082	Human angiogenesis
12	2004	99.6	390	22	AAE06610	Human protein havi
13	2004	99.6	390	22	AAB90818	Human shear stress
14	2003	99.6	389	21	AAY76303	Fragment of human
15	1738.5	86.4	370	22	AAB65832	Human INTERCEPT 25
16	1736.5	86.3	370	22	AAB65906	Human secreted pro
17	1734.5	86.2	370	22	AAB65904	Human secreted pro
18	1734.5	86.2	370	22	AAB65905	Human secreted pro
19	1734.5	86.2	370	22	AAB65907	Human secreted pro
20	1601.5	79.6	341	22	AAB65833	Murine mature INTE
21	1581	78.6	321	22	ABB11937	Human viral recept
22	1581	78.6	321	22	AAM40551	Human polypeptide
23	1579	78.5	325	21	AAY95024	Human clone vc51_1
24	1399	69.5	394	22	AAB65910	Murine secreted pr
25	1397	69.4	394	22	AAB65840	Murine INTERCEPT 2
26	1397	69.4	394	22	AAB65908	Murine secreted pr
27	1394	69.3	394	22	AAB65911	Murine secreted pr
28	1393	69.2	394	22	AAB65909	Murine secreted pr
29	1331	66.2	365	22	AAB65841	Murine mature INTE
30	1232	61.2	246	22	AAB65835	Murine INTERCEPT 2
31	1207	60.0	237	21	AAY76152	Human secreted pro
32	1107	55.0	220	22	AAB65872	Human INTERCEPT 25
33	1095	54.4	217	22	AAB65871	Human INTERCEPT 25
34	1027	51.0	206	22	AAB65870	Human INTERCEPT 25
35	965.5	48.0	212	20	AAY25748	Human secreted pro
36	890	44.2	177	22	AAB65867	Human INTERCEPT 25
37	833.5	41.4	249	22	AAB65843	Murine INTERCEPT 2
38	833	41.4	172	22	AAM38765	Human polypeptide
39	577	28.7	182	22	AAE05354	Mouse 10.3 kDa pro
40	467.5	23.2	120	22	AAB65846	Murine INTERCEPT 2
41	436	21.7	127	21	AAY95025	Human clone vc51_1
42	400.5	19.9	99	22	AAB65837	Murine INTERCEPT 2
43	400	19.9	80	22	AAB65838	Murine INTERCEPT 2
44	367.5	18.3	426	22	ABB10359	Human cDNA SEQ ID
45	361.5	18.0	376	19	AAW57213	Mouse coxsackievir

ALIGNMENTS

RESULT 1
AAY27096
ID AAY27096 standard; Protein; 390 AA.

XX

AC AAY27096;

XX

DT 18-OCT-1999 (first entry)

XX

DE Human viral receptor protein (ACVRP).

XX

KW Viral receptor protein; ACVRP; cancer; viral disorder; inflammation;
KW gene therapy; human.

XX

OS Homo sapiens.

XX

PN US5942606-A.

XX

PD 24-AUG-1999.

XX

PF 24-NOV-1997; 97US-0979424.

XX

PR 24-NOV-1997; 97US-0979424.

XX

PA (INCY-) INCYTE PHARM INC.

XX

PI Corley NC, Lal P;

XX

DR WPI; 1999-493538/41.
DR N-PSDB; AAX87000.

XX

PT Isolated and purified polynucleotide useful for treating or
PT preventing cancer, inflammation and viral disorders

XX

PS Claim 1; Fig 1A-D; 28pp; English.

XX

CC This represents a human viral receptor protein (ACVRP). The protein
CC can be expressed by standard recombinant methodology. ACVRP can be used
CC for treating and/or preventing cancer, a viral disorder or inflammation
CC through the administration of a vector expressing a polynucleotide which
CC is fully complementary to the present sequence. Polynucleotides encoding
CC ACVRP can be used for diagnostic purposes to quantitate ACVRP expression
CC in biopsied tissues and correlate expression with disease. They can be
CC used to distinguish between the absence, presence and excess expression
CC of ACVRP and to monitor levels during therapeutic intervention.
CC Hybridisation probes can be used for mapping the naturally occurring
CC genomic sequence and detect differences in the chromosomal location in
CC normal, carrier or affected individuals. ACVRP may be ligated to a
CC heterologous sequence to produce a fusion protein which can be used to
CC screen peptide libraries for inhibitors of ACVRP activity and to screen
CC for novel antiprotozoal and antifungal therapeutics. The expression
CC vectors which encode ACVRP can be used to deliver nucleotide sequences
CC to targeted organ, tissue or cell populations and complementary
CC polynucleotides to treat conditions associated with overexpression of
CC ACVRP by blocking transcription of the mRNA, modulating ACVRP activity
CC or regulating the gene function.

XX

SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 20; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;

Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mislpgplvtnllrflflglsalappsraqlqlhlpanrlqaveggevvlpawytlhgev 60

Qy     61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 sssqpwevpfvmwffkqkekedqvlsyingvttskpgvslvysmpsrnlslrleglqekd 120

Qy    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 sgpyscsvnvqdkqgksrghsiktlelnvlvppappscrlqgvphvganvtlscqsprsk 180

Qy    181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 pavqyqwdrqlpsfqtffapaldvirgslsltnlsssmagvyvckahnevgtaqcnvtle 240

Qy    241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 vstgpgaavvagavvgtlvglgllaglvllyhrrgkaleepandikedaiaprtlpwpks 300

Qy    301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 sdtisknqtlssvtsaralrpphgpprpgaltptpslssqalpsprlpttdgahpqpisp 360

Qy    361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
          ||||||||||||||||||||||||||||||
Db    361 ipggvsssglsrmgavpvmvpaqsqagslv 390
```

RESULT 2
AAY13351
ID AAY13351 standard; Protein; 390 AA.
XX
AC AAY13351;
XX
DT 25-JUN-1999 (first entry)
XX
DE Amino acid sequence of protein PRO246.
XX
KW Secreted protein; transmembrane protein; human; enterocolitis;
KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW congenital microvillus atrophy; skin disease; cell growth;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
KW anti-thrombotic; wound healing; tissue repair.
XX
OS Homo sapiens.
XX
PN WO9914328-A2.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-US19330.
XX

PR 25-NOV-1997; 97US-0066840.
PR 17-SEP-1997; 97US-0059113.
PR 17-SEP-1997; 97US-0059115.
PR 17-SEP-1997; 97US-0059117.
PR 17-SEP-1997; 97US-0059119.
PR 17-SEP-1997; 97US-0059121.
PR 17-SEP-1997; 97US-0059122.
PR 17-SEP-1997; 97US-0059184.
PR 18-SEP-1997; 97US-0059263.
PR 18-SEP-1997; 97US-0059266.
PR 15-OCT-1997; 97US-0062125.
PR 17-OCT-1997; 97US-0062285.
PR 17-OCT-1997; 97US-0062287.
PR 21-OCT-1997; 97US-0063486.
PR 24-OCT-1997; 97US-0062814.
PR 24-OCT-1997; 97US-0062816.
PR 24-OCT-1997; 97US-0063045.
PR 24-OCT-1997; 97US-0063120.
PR 24-OCT-1997; 97US-0063121.
PR 24-OCT-1997; 97US-0063127.
PR 24-OCT-1997; 97US-0063128.
PR 27-OCT-1997; 97US-0063329.
PR 27-OCT-1997; 97US-0063327.
PR 28-OCT-1997; 97US-0063541.
PR 28-OCT-1997; 97US-0063542.
PR 28-OCT-1997; 97US-0063544.
PR 28-OCT-1997; 97US-0063549.
PR 28-OCT-1997; 97US-0063550.
PR 28-OCT-1997; 97US-0063564.
PR 29-OCT-1997; 97US-0063435.
PR 29-OCT-1997; 97US-0063704.
PR 29-OCT-1997; 97US-0063732.
PR 29-OCT-1997; 97US-0063738.
PR 29-OCT-1997; 97US-0063734.
PR 29-OCT-1997; 97US-0064215.
PR 29-OCT-1997; 97US-0063735.
PR 31-OCT-1997; 97US-0063870.
PR 31-OCT-1997; 97US-0064103.
PR 03-NOV-1997; 97US-0064248.
PR 07-NOV-1997; 97US-0064809.
PR 12-NOV-1997; 97US-0065186.
PR 17-NOV-1997; 97US-0065846.
PR 18-NOV-1997; 97US-0065693.
PR 21-NOV-1997; 97US-0066120.
PR 21-NOV-1997; 97US-0066364.
PR 24-NOV-1997; 97US-0066772.
PR 24-NOV-1997; 97US-0066466.
PR 24-NOV-1997; 97US-0066770.
PR 24-NOV-1997; 97US-0066511.
PR 24-NOV-1997; 97US-0066453.
XX
PA (GETH) GENENTECH INC.
XX
PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
XX
DR WPI; 1999-229533/19.
DR N-PSDB; AAX52221.
XX

PT New isolated human genes and polypeptides used in, e.g. treatment of
PT gastrointestinal ulceration
XX
PS Claim 12; Fig 17; 320pp; English.
XX
CC AAY13344-403 represent secreted and transmembrane human proteins.
CC The cDNA sequences are obtained from cDNA libraries, prepared from
CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
CC The encoded polypeptides have specific uses based on their homology to
CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders
CC associated with the preservation and maintenance of gastrointestinal
CC mucosa and the repair of acute and chronic mucosal lesions
CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
CC ulceration and congenital microvillus atrophy), skin diseases associated
CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),
CC potent effects on cell growth and development, diseases related to
CC growth or survival of nerve cells including Parkinson's disease,
CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as
CC for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used
CC as a target for anti-tumor drugs. PRO533 may be used in the treatment
CC of Usher Syndrome or Atrophia areata; PRO269 can be used as an
CC anti-thrombotic agent; PRO287 polypeptides and portions may have
CC therapeutic applications in wound healing and tissue repair; PRO317 can
CC be used for treating problems of the kidney, uterus, endometrium, blood
CC vessels, or related tissue, e.g. in the heart of genital tract.
XX
SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 20; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mislpgplvtnllrflflglsalappsraqlqlhlpanrlqaveggevvlpawytlhgev 60

Qy     61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 sssqpwevpfvmwffkqkekedqvlsyingvttskpgvslvysmpsrnlslrleglqekd 120

Qy    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 sgpyscsvnvqdkqgksrghsiktlelnvlvppappscrlqgvphvganvtlscqsprsk 180

Qy    181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 pavqyqwdrqlpsfqtffapaldvirgslsltnlsssmagvyvckahnevgtaqcnvtle 240

Qy    241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 vstgpgaavvagavvgtlvglgllaglvllyhrrgkaleepandikedaiaprtlpwpks 300

Qy    301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 sdtiskngtlssvtsaralrpphgpprpgaltptpslssqalpsprlpttdgahpqpisp 360
```

```
Qy     361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
           ||||||||||||||||||||||||||||||
Db     361 ipggvsssglsrmgavpvmvpaqsqagslv 390
```

RESULT 3
AAY05286
ID AAY05286 standard; Protein; 390 AA.
XX
AC AAY05286;
XX
DT 22-JUN-1999 (first entry)
XX
DE EGF-like homologue PRO246.
XX
KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;
KW EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue;
KW FGF-8 homologue.
XX
OS Homo sapiens.
XX
PN WO9914327-A2.
XX
PD 25-MAR-1999.
XX
PF 10-SEP-1998; 98WO-US18824.
XX
PR 25-NOV-1997; 97US-0066840.
PR 17-SEP-1997; 97US-0059114.
PR 17-SEP-1997; 97US-0059117.
PR 18-SEP-1997; 97US-0059263.
PR 15-OCT-1997; 97US-0062125.
PR 17-OCT-1997; 97US-0062285.
PR 17-OCT-1997; 97US-0062287.
PR 24-OCT-1997; 97US-0062816.
PR 29-OCT-1997; 97US-0063704.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney A, Hillan K, Lawrence DA;
PI Roy M, Wood WI;
XX
DR WPI; 1999-229532/19.
DR N-PSDB; AAX28436.
XX
PT Antibodies against specific proteins overexpressed in tumours
XX
PS Example 1; Fig 27; 130pp; English.
XX
CC This sequence represents the EGF-like homologue PRO246.
CC The invention relates to antibodies (Ab) that bind to any of the
CC polypeptides (I) designated PRO187; PRO533; PRO214; PRO240; PRO211;
CC PRO230; PRO261; PRO246 or EBAF-2. The Ab, or other agents that inhibit
CC expression and/or activity of (I) are used: (i) to inhibit growth of
CC tumours; and (ii) as diagnostic/prognostic reagents for detection or
CC quantification of (I) in cells or tissues, by standard immunoassays,
with
CC overexpression being indicative of cancer. For therapeutic use, the Ab
CC may be conjugated to a toxin, chemotherapeutic agent or radioisotope.
CC Genes expressing (I), many of which are growth factor homologues, are
CC overexpressed in some cases of cancer.
XX
SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 20; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mislpgplvtnllrflflglsalappsraqlqlhlpanrlqaveggevvlpawytlhgev 60

Qy      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sssqpwevpfvmwffkqkekedqvlsyingvttskpgvslvysmpsrnlslrleglqekd 120

Qy     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 sgpyscsvnvqdkqgksrghsiktlelnvlvppappscrlqgvphvganvtlscqsprsk 180

Qy     181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 pavqyqwdrqlpsfqtffapaldvirgslsltnlsssmagvyvckahnevgtaqcnvtle 240

Qy     241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 vstgpgaavvagavvgtlvglgllaglvllyhrrgkaleepandikedaiaprtlpwpks 300

Qy     301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 sdtisknqtlssvtsaralrpphgpprpgaltptpslssqalpsprlpttdgahpqpisp 360

Qy     361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
           ||||||||||||||||||||||||||||||
Db     361 ipggvsssglsrmgavpvmvpaqsqagslv 390
```

RESULT 4
AAY88574
ID AAY88574 standard; Protein; 390 AA.
XX
AC AAY88574;
XX
DT 09-AUG-2000 (first entry)
XX
DE Human PRO246 amino acid sequence.
XX
KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;
KW PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human;
KW cell growth; proliferation; cell surface virus receptor; ADEPT;
KW antibody dependent enzyme mediated prodrug therapy.
XX

OS Homo sapiens.
XX
PN WO200015666-A2.
XX
PD 23-MAR-2000.
XX
PF 08-SEP-1999; 99WO-US20594.
XX
PR 10-SEP-1998; 98US-0099803.
PR 10-SEP-1998; 98WO-US18824.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI, Botstein D;
XX
DR WPI; 2000-271386/23.
DR N-PSDB; AAA30052.
XX
PT New isolated antibodies which bind to specific polypeptides used for
PT diagnosis and treatment of neoplastic cell growth and proliferation -
XX
PS Example 8; Fig 16; 200pp; English.
XX
CC This sequence represents a human PRO246 amino acid sequence. PRO246 is
CC probably a cell surface virus receptor. The invention relates to
isolated
CC antibodies which bind to a polypeptide. The "PRO" polypeptides are
CC encoded by genes which are over expressed in the genome of tumour cells.
CC Vectors and host cells comprising the nucleic acid encoding the
CC antibodies are used in the production of the antibodies. The antibodies
CC and nucleic acids encoding them are used for diagnosing a tumour in a
CC mammal. The antibodies are used for inhibiting the growth of tumour
cells
CC and identifying compounds that inhibit a biological or immunological
CC activity of and/or expression of a PRO187, PRO533, PRO214, PRO240,
CC PRO211, PRO230, PRO261, PRO246 or PRO317 polypeptide. The antibody can
be
CC used in antibody dependent enzyme mediated prodrug therapy (ADEPT) by
CC conjugating the antibody to a prodrug-activating enzyme which converts
a
CC prodrug to an anti-cancer drug. The antibodies can be fluorescently
CC labelled and monitored by light microscopy, flow cytometry or
fluorimetry
CC for diagnosis and prognosis of tumours.
XX
SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 21; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps
0;

```
Qy       1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mislpgplvtnllrflflglsalappsraqlqlhlpanrlqaveggevvlpawytlhgev 60

Qy      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sssqpwevpfvmwffkqkekedqvlsyingvttskpgvslvysmpsrnlslrleglqekd 120

Qy     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 sgpyscsvnvqdkqgksrghsiktlelnvlvppappscrlqgvphvganvtlscqsprsk 180

Qy     181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 pavqyqwdrqlpsfqtffapaldvirgslsltnlsssmagvyvckahnevgtaqcnvtle 240

Qy     241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 vstgpgaavvagavvgtlvglgllaglvllyhrrgkaleepandikedaiaprtlpwpks 300

Qy     301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 sdtiskngtlssvtsaralrpphgpprpgaltptpslssqalpsprlpttdgahpqpisp 360

Qy     361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
           |||||||||||||||||||||||||||||
Db     361 ipggvsssglsrmgavpvmvpaqsqagslv 390
```

RESULT 5
AAY94999
ID AAY94999 standard; Protein; 390 AA.
XX
AC AAY94999;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human secreted protein vc51_1, SEQ ID NO:38.
XX
KW Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW neurodegenerative disease; asthma; contraceptive.
XX
OS Homo sapiens.
XX
PN WO200011015-A1.
XX
PD 02-MAR-2000.
XX
PF 24-AUG-1999; 99WO-US19351.
XX
PR 24-AUG-1998; 98US-0097638.
PR 24-AUG-1998; 98US-0097659.
PR 09-SEP-1998; 98US-0099618.
PR 28-SEP-1998; 98US-0102092.
PR 25-NOV-1998; 98US-0109978.
PR 23-DEC-1998; 98US-0113645.
PR 23-DEC-1998; 98US-0113646.
PR 23-AUG-1999; 99US-0379246.
XX
PA (ALPH-) ALPHAGENE INC.
XX

PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-224657/19.
XX
PT New secreted or transmembrane proteins and polynucleotides encoding
PT them, useful for treating neurodegenerative disorders, autoimmune
PT diseases and cancer -
XX
PS Claim 47; Page 296-297; 357pp; English.
XX
CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted
CC proteins of the invention include those that are thought to be only
CC partially secreted, i.e., transmembrane proteins. The proteins of the
CC invention may exhibit one or more activities selected from the
following:
CC cytokine activity; cell proliferation; differentiation; immune
CC modulation; haematopoiesis regulation; tissue growth activity;
CC activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic
CC and thrombolytic activity; anti-inflammatory activity; and tumour
CC inhibition activity. The proteins may be administered to patients as
CC vaccines, and the nucleotides may be used as part of a gene therapy
CC regime. Diseases or conditions that may be treated using the proteins or
CC nucleotides of the invention include autoimmune diseases; genetic
CC disorders; haemophilia; cardiovascular diseases; cancer; bacterial,
CC fungal and viral infections, especially HIV; multiple sclerosis;
CC rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome;
CC insulin dependent diabetes mellitus; and allergic reactions such as
CC asthma and anaemia. They may also be used for treating wounds, burns,
CC ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's
CC disease, Parkinson's disease, Huntington's disease and amyotrophic
CC lateral sclerosis (ALS). Proteins with activin/inhibin activity may
CC additionally be useful as contraceptives. Nucleic acid sequences of the
CC invention may be used in chromosome mapping, and as a source of
CC diagnostic primers and probes. The present sequence represents one of
the
CC 40 proteins of the invention.
XX
SQ Sequence 390 AA;

  Query Match 100.0%; Score 2012; DB 21; Length 390;
  Best Local Similarity 100.0%; Pred. No. 5.8e-143;
  Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps
0;

Qy   1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 mislpgplvtnllrflflglsalappsraqlqlhlpanrlqaveggevvlpawytlhgev 60

Qy   61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 sssqpwevpfvmwffkqkekedqvlsyingvttskpgvslvysmpsrnlslrleglqekd 120

Qy 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 sgpyscsvnvqdkqgksrghsiktlelnvlvppappscrlqgvphvganvtlscqsprsk 180

Qy 181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 pavqyqwdrqlpsfqtffapaldvirgslsltnlsssmagvyvckahnevgtaqcnvtle 240

Qy 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 vstgpgaavvagavvgtlvglgllaglvllyhrrgkaleepandikedaiaprtlpwpks 300

Qy 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 sdtiskngtlssvtsaralrpphgpprpgaltptpslssqalpsprlpttdgahpqpisp 360

Qy 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
          ||||||||||||||||||||||||||||||
Db 361 ipggvsssglsrmgavpvmvpaqsqagslv 390

RESULT 6
AAU12340
ID AAU12340 standard; Protein; 390 AA.
XX
AC AAU12340;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO246 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal
muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32678.
XX
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR N-PSDB; AAS21412.
XX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical -
XX
PS Claim 12; Fig 338; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 22; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 misLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60

Qy      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sssqpwevpfvmwffkqkekedqvlsyingvttskpgvslvysmpsrnlslrleglqekd 120

Qy     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 sgpyscsvnvqdkqgksrghsiktlelnvlvppappscrlqgvphvganvtlscqsprsk 180

Qy     181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 pavqyqwdrqlpsfqtffapaldvirgslsltnlsssmagvyvckahnevgtaqcnvtle 240

Qy     241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 vstgpgaavvagavvgtlvglgllaglvllyhrrgkaleepandikedaiaprtlpwpks 300

Qy     301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 sdtiskngtlssvtsaralrpphgpprpgaltptpslssqalpsprlpttdgahpqpisp 360

Qy     361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
           ||||||||||||||||||||||||||||||
Db     361 ipggvsssglsrmgavpvmvpaqsqagslv 390
```

RESULT 7
AAB88358
ID AAB88358 standard; Protein; 390 AA.
XX
AC AAB88358;
XX
DT 23-MAY-2001 (first entry)
XX
DE Human membrane or secretory protein clone PSEC0086.
XX
KW Human; secretory protein; membrane protein; vaccine; gene therapy;
KW rheumatoid arthritis; diabetes.
XX
OS Homo sapiens.
XX
PN EP1067182-A2.
XX
PD 10-JAN-2001.
XX
PF 07-JUL-2000; 2000EP-0114090.
XX
PR 08-JUL-1999; 99JP-0194179.
PR 11-JAN-2000; 2000JP-0118775.
PR 02-MAY-2000; 2000JP-0183766.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX
DR WPI; 2001-093989/11.
DR N-PSDB; AAF93785.

XX

PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development -

XX

PS Claim 1; SEQ ID 84; 609pp + CD ROM; English.

XX

CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by
CC AAB88317 - AAB88419. Included in the invention are primers
CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate
the
CC cDNA sequences of the invention. The invention also includes methods for
CC the production of antibodies directed against the proteins, and cDNA
CC sequences, which can be used in vaccines. The polynucleotide sequences
CC can be used in gene therapy. The polynucleotide sequences and the
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate secretory
CC protein/membrane protein expression. The nucleic acids and complementary
CC sequences may also be used as DNA probes in diagnostic assays
CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC presence of similar nucleic acid sequences in samples. They may also be
CC used to study the expression and function of secretory proteins/membrane
CC polypeptides and their role in metabolism. The polypeptides may be used
CC as antigens in the production of antibodies against them and in assays
to
CC identify modulators (agonists and antagonists) of expression and
CC activity. The antibodies and antagonists may also be used as therapeutic
CC agents to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA). Examples of diseases which may be treated include rheumatoid
CC arthritis and diabetes.

XX

SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 22; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps
0;

```
Qy      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mislpgplvtnllrflflglsalappsraqlqlhlpanrlqaveggevvlpawytlhgev 60

Qy     61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 sssqpwevpfvmwffkqkekedqvlsyingvttskpgvslvysmpsrnlslrleglqekd 120

Qy    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 sgpyscsvnvqdkqgksrghsiktlelnvlvppappscrlqgvphvganvtlscqsprsk 180

Qy    181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 pavqyqwdrqlpsfqtffapaldvirgslsltnlsssmagvyvckahnevgtaqcnvtle 240

Qy    241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 vstgpgaavvagavvgtlvglgllaglvllyhrrgkaleepandikedaiaprtlpwpks 300

Qy    301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 sdtiskngtlssvtsaralrpphgpprpgaltptpslssqalpsprlpttdgahpqpisp 360

Qy    361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
          ||||||||||||||||||||||||||||||
Db    361 ipggvsssglsrmgavpvmvpaqsqagslv 390
```

RESULT 8
AAB68599
ID AAB68599 standard; Protein; 390 AA.
XX
AC AAB68599;
XX
DT 27-APR-2001 (first entry)
XX
DE PRO246.
XX
KW Cytostatic; PRO protein; tumour; cancer.
XX
OS Homo sapiens.
XX
PN WO200105836-A1.
XX
PD 25-JAN-2001.
XX
PF 20-DEC-1999; 99WO-US30999.
XX
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28564.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI;
XX
DR WPI; 2001-091968/10.
DR N-PSDB; AAF60372.
XX
PT New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533,
PT useful for diagnosing and treating cancers -
XX
PS Claim 61; Fig 16; 196pp; English.
XX
CC The present invention relates to PRO proteins and coding sequences. The
CC present sequence is one such PRO protein. It was found that the PRO
genes
CC are amplified in the genome of tumour cells. The gene amplification is

```
CC   expected to be associated with the overexpression of the gene product
and
CC   contributes to tumourigenesis. Therefore, antagonists of PRO proteins
are
CC   useful for the treatment of benign or malignant tumours, leukaemias,
CC   lymphoid malignancies and other disorders such as neuronal, glial,
CC   astrocytal, hypothalamic, glandular, epithelial, inflammatory and
CC   immunologic disorders.
XX
SQ   Sequence   390 AA;


  Query Match             100.0%;  Score 2012;  DB 22;  Length 390;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-143;
  Matches  390;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy       1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mislpgplvtnllrflflglsalappsraqlqlhlpanrlqaveggevvlpawytlhgev 60

Qy      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sssqpwevpfvmwffkqkekedqvlsyingvttskpgvslvysmpsrnlslrleglqekd 120

Qy     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 sgpyscsvnvqdkqgksrghsiktlelnvlvppappscrlqgvphvganvtlscqsprsk 180

Qy     181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 pavqyqwdrqlpsfqtffapaldvirgslsltnlsssmagvyvckahnevgtaqcnvtle 240

Qy     241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 vstgpgaavvagavvgtlvglgllaglvllyhrrgkaleepandikedaiaprtlpwpks 300

Qy     301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 sdtiskngtlssvtsaralrpphgpprpgaltptpslssqalpsprlpttdgahpqpisp 360

Qy     361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
           |||||||||||||||||||||||||||||
Db     361 ipggvsssglsrmgavpvmvpaqsqagslv 390


RESULT   9
AAB31207
ID   AAB31207 standard; Protein; 390 AA.
XX
AC   AAB31207;
XX
DT   20-APR-2001  (first entry)
XX
DE   Amino acid sequence of human polypeptide PRO246.
XX
KW   Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW     PRO185;  PRO210;  PRO215;  PRO217;  PRO242;  PRO288;  PRO365;  PRO1361;
PRO1308;
KW   PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW   PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW   PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW   PRO6309; cell death; genetic disorder; transgenic animal; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..29
FT                   /note= "signal peptide"
FT   Modified-site   90..96
FT                   /note= "N-myristoylation site"
FT   Modified-site   108..112
FT                   /note= "N-glycosylation site"
FT   Modified-site   167..173
FT                   /note= "N-myristoylation site"
FT   Modified-site   169..173
FT                   /note= "N-glycosylation site"
FT   Modified-site   213..217
FT                   /note= "N-glycosylation site"
FT   Modified-site   220..226
FT                   /note= "N-myristoylation site"
FT   Modified-site   231..237
FT                   /note= "N-myristoylation site"
FT   Modified-site   236..240
FT                   /note= "N-glycosylation site"
FT   Domain          245..267
FT                   /note= "transmembrane protein"
FT   Modified-site   252..258
FT                   /note= "N-myristoylation site"
FT   Modified-site   256..262
FT                   /note= "N-myristoylation site"
FT   Modified-site   262..268
FT                   /note= "N-myristoylation site"
FT   Modified-site   307..311
FT                   /note= "N-glycosylation site"
FT   Modified-site   308..314
FT                   /note= "N-myristoylation site"
FT   Modified-site   363..369
FT                   /note= "N-myristoylation site"
FT   Modified-site   364..370
FT                   /note= "N-myristoylation site"
XX
PN   WO200077037-A2.
XX
PD   21-DEC-2000.
XX
PF   22-MAY-2000; 2000WO-US14042.
XX
PR   15-JUN-1999;   99US-0139695.
PR   20-JUL-1999;   99US-0145070.
PR   26-JUL-1999;   99US-0145698.
PR   17-AUG-1999;   99US-0149396.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
```

```
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28301.
PR   02-DEC-1999;   99WO-US28565.
PR   07-DEC-1999;   99US-0169495.
PR   05-JAN-2000; 2000WO-US00219.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   20-MAR-2000; 2000WO-US07377.
PR   30-MAR-2000; 2000WO-US08439.
PR   15-MAY-2000; 2000WO-US13358.
PR   17-MAY-2000; 2000WO-US13705.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2001-050091/06.
DR   N-PSDB; AAC87040.
XX
PT   Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT   transmembrane polypeptide is useful for gene therapy and identification
PT   of related polypeptides -
XX
PS   Claim 12; Fig 58; 244pp; English.
XX
CC   The present sequence represents a human secreted and transmembrane
CC   polypeptide. The specification describes human polypeptides, designated
CC   PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC   PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
CC   PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC   PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC   PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC   can be modulated with agents that bind to these polypeptides, resulting
CC   in the death of the cells. The polynucleotides encoding these
CC   polypeptides are useful in the recombinant production of the
CC   polypeptides, as a hybridisation probe to screen libraries to isolate
CC   homologous sequences, or to map the gene. They may also be used for
CC   analysing genetic disorders, and to produce transgenic animals which are
CC   useful for the development and screening of therapeutically useful
CC   reagents. The polynucleotides can also be used in gene therapy e.g. to
CC   replace a defective gene.
XX
SQ   Sequence   390 AA;


  Query Match             100.0%;  Score 2012;  DB 22;  Length 390;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-143;
  Matches  390;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy       1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
                                                                        
Db       1 misLpgplvtnllrflflglsalappsraqlqlhlpanrlqaveggevvlpawytlhgev 60

Qy      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
                                                                        
Db      61 sssqpwevpfvmwffkqkekedqvlsyingvttskpgvslvysmpsrnlslrleglqekd 120

Qy     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
                                                                        
Db     121 sgpyscsvnvqdkqgksrghsiktlelnvlvppappscrlqgvphvganvtlscqsprsk 180

Qy     181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
                                                                        
Db     181 pavqyqwdrqlpsfqtffapaldvirgslsltnlsssmagvyvckahnevgtaqcnvtle 240

Qy     241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
                                                                        
Db     241 vstgpgaavvagavvgtlvglgllaglvllyhrrgkaleepandikedaiaprtlpwpks 300

Qy     301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
                                                                        
Db     301 sdtiskngtlssvtsaralrpphgpprpgaltptpslssqalpsprlpttdgahpqpisp 360

Qy     361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
                                           
Db     361 ipggvsssglsrmgavpvmvpaqsqagslv 390


RESULT  10
AAB80219
ID   AAB80219 standard; Protein; 390 AA.
XX
AC   AAB80219;
XX
DT   24-APR-2001  (first entry)
XX
DE   Human PRO246 protein.
XX
KW   Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW   antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW   antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW   antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW   ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW   ischaemia; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200104311-A1.
XX
PD   18-JAN-2001.
XX
PF   22-FEB-2000; 2000WO-US04414.
XX
PR   07-JUL-1999;   99US-0143048.
PR   26-JUL-1999;   99US-0145698.
PR   28-JUL-1999;   99US-0146222.
PR   08-SEP-1999;   99WO-US20594.
PR   13-SEP-1999;   99WO-US20944.
```

PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 99WO-US00219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2001-081051/09.
DR N-PSDB; AAF72379.
XX
PT Sixty one nucleic acids encoding PRO polypeptides which are useful in
PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
PT Alzheimer's disease) -
XX
PS Claim 1; Fig 17; 393pp; English.
XX
CC The present sequence is one of sixty one novel secreted and
CC transmembrane PRO polypeptides. The PRO polypeptides are
CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
CC squamous cell carcinoma), gastrointestinal disorders (e.g.
CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
CC endometrial bleeding angiogenesis, ischaemias such as coronary
CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
CC diabetes and retinal disorders such as retinitis pigmentosum.
CC The PRO nucleic acids have applications in molecular biology, including
CC use as hybridization probes, and in chromosome and gene mapping.
XX
SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 22; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mislpgplvtnllrflflglsalappsraqlqlhlpanrlqaveggevvlpawytlhgev 60

Qy     61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 sssqpwevpfvmwffkqkekedqvlsyingvttskpgvslvysmpsrnlslrleglqekd 120

Qy    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 sgpyscsvnvqdkqgksrghsiktlelnvlvppappscrlqgvphvganvtlscqsprsk 180

Qy    181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 pavqyqwdrqlpsfqtffapaldvirgslsltnlsssmagvyvckahnevgtaqcnvtle 240

Qy    241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 vstgpgaavvagavvgtlvglgllaglvllyhrrgkaleepandikedaiaprtlpwpks 300

Qy    301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 sdtisksngtlssvtsaralrpphgpprpgaltptpslssqalpsprlpttdgahpqpisp 360

Qy    361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
          |||||||||||||||||||||||||||||
Db    361 ipggvsssglsrmgavpvmvpaqsqagslv 390
```

RESULT 11
AAB53082
ID AAB53082 standard; Protein; 390 AA.
XX
AC AAB53082;
XX
DT 28-FEB-2001 (first entry)
XX
DE Human angiogenesis-associated protein PRO246, SEQ ID NO:96.
XX
KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
KW gene therapy; transgenic animal.
XX
OS Homo sapiens.
XX
PN WO200053753-A2.
XX
PD 14-SEP-2000.
XX
PF 05-JAN-2000; 2000WO-US00219.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 14-MAY-1999; 99US-0134287.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.

PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2001-090793/10.
DR N-PSDB; AAC97441.
XX
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing
PT genetic disorders and treating cardiovascular, endothelial or
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -
XX
PS Claim 69; Fig 38; 293pp; English.
XX
CC The invention relates to novel human angiogenesis-associated proteins
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
CC PRO proteins. The invention also relates to vectors and host cells
CC comprising a PRO nucleic acid, the recombinant production of a PRO
CC protein, PRO antibodies specific for a PRO protein, fusion proteins
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
CC compounds which inhibit the expression of a PRO gene. The invention
CC additionally encompasses methods of identifying modulators of PRO
CC expression or activity; diagnosing a cardiovascular, endothelial or
CC angiogenic disorder, or a susceptibility to such a disorder by detecting
CC mutations in a PRO gene, or the expression level of a PRO gene within a
CC particular tissue; treating a cardiovascular, endothelial or angiogenic
CC disorder via the administration of a PRO protein, PRO nucleic acid, or
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising
a
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
CC administration of a PRO protein, or an agonist or antagonist thereof.
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
CC agonists and PRO antagonists may be used as therapeutic agents to treat
CC cardiovascular, endothelial or angiogenic disorders, such as
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
CC disease, or stroke. PRO nucleic acids are additionally useful in the
CC recombinant production of PRO proteins, as hybridisation probes to
CC screen libraries to isolate cDNAs with sequence identity to PRO
proteins,
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in
CC gene therapy. PRO nucleic acids can also be used to produce transgenic
CC animals useful for the development and screening of potential
CC therapeutic agents. The present sequence represents a PRO protein of the
CC invention.
XX
SQ Sequence 390 AA;

Query Match 100.0%; Score 2012; DB 22; Length 390;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps
0;

```
Qy      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mislpgplvtnllrflflglsalappsraqlqlhlpanrlqaveggevvlpawytlhgev 60

Qy     61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 sssqpwevpfvmwffkqkekedqvlsyingvttskpgvslvysmpsrnlslrleglqekd 120

Qy    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 sgpyscsvnvqdkqgksrghsiktlelnvlvppappscrlqgvphvganvtlscqsprsk 180

Qy    181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 pavqyqwdrqlpsfqtffapaldvirgslsltnlsssmagvyvckahnevgtaqcnvtle 240

Qy    241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 vstgpgaavvagavvgtlvglgllaglvllyhrrgkaleepandikedaiaprtlpwpks 300

Qy    301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 sdtisknqtlssvtsaralrpphgpprpgaltptpslssqalpsprlpttdgahpqpisp 360

Qy    361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
          ||||||||||||||||||||||||||||||
Db    361 ipggvsssglsrmgavpvmvpaqsqagslv 390
```

RESULT 12
AAE06610
ID AAE06610 standard; Protein; 390 AA.
XX
AC AAE06610;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human protein having hydrophobic domain, HP10801.
XX
KW Human; hydrophobic domain; gene therapy; nutritional supplement;
KW cell proliferation; immunomodulatory; autoimmune disorder;
antimicrobial;
KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
KW haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
KW contraceptive; antiinfertility; antiinflammatory.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT /label= Signal_peptide
FT Protein 31..390

FT /note= "Mature human protein with hydrophobic domain"
XX
PN WO200149728-A2.
XX
PD 12-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-JP09359.
XX
PR 06-JAN-2000; 2000JP-0000585.
PR 06-JAN-2000; 2000JP-0000588.
PR 11-JAN-2000; 2000JP-0002299.
PR 03-FEB-2000; 2000JP-0026862.
PR 03-MAR-2000; 2000JP-0058367.
XX
PA (PROT-) PROTEGENE INC.
PA (SAGA) SAGAMI CHEM RES CENT.
XX
PI Kato S, Kimura T;
XX
DR WPI; 2001-418355/44.
DR N-PSDB; AAD12605.
XX
PT Human proteins with hydrophobic domains and the nucleic acids encoding
PT them, useful for preventing diagnosing and treating e.g. cancer,
PT Alzheimer's and inflammation -
XX
PS Claim 1; Page 448-450; 563pp; English.
XX
CC The present sequence is human protein with hydrophobic domain,
CC HP10801. The polynucleotide and polypeptide of the invention
CC may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The polynucleotides
CC may be used to produce the polypeptide, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the protein. The
CC polynucleotides and its complementary sequences may also be used as DNA
CC probes in diagnostic assays and also used in gene therapy. The
CC polypeptides may also be used as antigens in the production of antibodies
CC and in assays to identify modulators of polypeptide expression and
CC activity. The polypeptides and nucleic acids may be used as nutritional
CC supplements, to modulate cytokine and cell proliferation activity, to
CC modulate immune stimulation or suppression (e.g. for the treatment of
CC microbial infections and autoimmune disorders such as multiple sclerosis,
CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
CC haematopoiesis, to modulate tissue growth activity (e.g. for the
CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
CC disease), to modulate activin and inhibin activity (e.g. for controlling
CC fertility), to modulate chemotactic and chemokinetic activity, to
CC modulate haemostatic and thrombolytic activity, to modulate receptor
CC ligand activity, to modulate inflammation and to inhibit tumour growth.
XX
SQ Sequence 390 AA;

Query Match 99.6%; Score 2004; DB 22; Length 390;
Best Local Similarity 99.7%; Pred. No. 2.3e-142;
Matches 389; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mislpgplvtnllrflflglsalappsraqlqlhlpanrlqaveggevvlpawytlhgev 60

Qy     61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 sssqpwevpfvmwffkqkekedqvlsyingvttskpgvslvysmpsrnlslrleglqekd 120

Qy    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 sgpyscsvnvqdkqgksrghsiktlelnvlvppappscrlqgvphvganvtlscqsprsk 180

Qy    181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 pavqyqwdrqlpsfqtffapaldvirgslsltnlsssmagvyvckahnevgtaqcnvtle 240

Qy    241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    241 vstgpgaavvagavvgtlvglgllaglvllyhcrgkaleepandikedaiaprtlpwpks 300

Qy    301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 sdtisknqtlssvtsaralrpphgpprpgaltptpslssqalpsprlpttdgahpqpisp 360

Qy    361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
          |||||||||||||||||||||||||||||
Db    361 ipggvsssglsrmgavpvmvpaqsqagslv 390
```

RESULT 13
AAB90818
ID AAB90818 standard; Protein; 390 AA.
XX
AC AAB90818;
XX
DT 15-JUN-2001 (first entry)
XX
DE Human shear stress-response protein SEQ ID NO: 144.
XX
KW Human; shear stress-response protein; vascular disease;
KW arteriosclerosis.
XX
OS Homo sapiens.
XX
PN WO200125427-A1.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-JP06840.
XX
PR 01-OCT-1999; 99JP-0280976.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (NOJI/) NOJIMA H.
XX

PI Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
PI Kuga T, Sekine S, Nakamura Y, Sugano S;
XX
DR WPI; 2001-266308/27.
DR N-PSDB; AAH02949.
XX
PT DNA sequences, proteins encoded by them and antibodies against them
PT useful in diagnosis and treatment of vascular disease caused by
PT arteriosclerosis -
XX
PS Claim 35; Page 599-601; 678pp; Japanese.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human shear stress response proteins. These are useful in the
CC diagnosis, treatment and screening of vascular diseases caused by
CC arteriosclerosis, including heart failure, post-PTCA restenosis and
CC hypertension.
XX
SQ Sequence 390 AA;

Query Match 99.6%; Score 2004; DB 22; Length 390;
Best Local Similarity 99.7%; Pred. No. 2.3e-142;
Matches 389; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mislpgplvtnllrflflglsalappsraqlqlhlpanrlqaveggevvlpawytlhgev 60

Qy      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sssqpwevpfvmwffkqkekedqvlsyingvttskpgvslvysmpsrnlslrleglqekd 120

Qy     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 sgpyscsvnvqdkqgksrghsiktlelnvlvppappscrlqgvphvganvtlscqsprsk 180

Qy     181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 pavqyqwdrqlpsfqtffapaldvirgslsltnlsssmagvyvckahnevgtaqcnvtle 240

Qy     241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 vstgpgaavvagavvgtlvglgllaglvllyhrrgkaleepandikedaiaprtlpwpks 300

Qy     301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     301 sdtisksngtlssvtsaralwpphgpprpgaltptpslssqalpsprlpttdgahpqpisp 360

Qy     361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
           ||||||||||||||||||||||||||||||
Db     361 ipggvsssglsrmgavpvmvpaqsqagslv 390
```

RESULT 14
AAY76303
ID AAY76303 standard; Protein; 389 AA.
XX
AC AAY76303;
XX
DT 23-MAR-2000 (first entry)
XX
DE Fragment of human secreted protein encoded by gene 29.
XX
KW Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW therapy.
XX
OS Homo sapiens.
XX
PN WO9958660-A1.
XX
PD 18-NOV-1999.
XX
PF 06-MAY-1999; 99WO-US09847.
XX
PR 12-MAY-1998; 98US-0085093.
PR 12-MAY-1998; 98US-0085094.
PR 12-MAY-1998; 98US-0085105.
PR 12-MAY-1998; 98US-0085180.
PR 18-MAY-1998; 98US-0085906.
PR 18-MAY-1998; 98US-0085920.
PR 18-MAY-1998; 98US-0085921.
PR 18-MAY-1998; 98US-0085922.
PR 18-MAY-1998; 98US-0085923.
PR 18-MAY-1998; 98US-0085924.
PR 18-MAY-1998; 98US-0085928.
PR 18-MAY-1998; 98US-0085925.
PR 18-MAY-1998; 98US-0085927.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR;
PI Lafleur DW, Endress GA, Ebner R;
XX
DR WPI; 2000-062296/05.
XX
PT New isolated human genes and the secreted polypeptides they encode,
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders -
XX
PS Disclosure; Page 440-441; 475pp; English.
XX
CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
CC AAY76124 to AAY76223 are the secreted proteins encoded by the 97 human
CC genes. This sequence represents a fragment of one of the human secreted
CC proteins. The genes and their corresponding secreted polypeptides are
CC useful for preventing, treating or ameliorating medical conditions,
CC e.g. by protein or gene therapy. Also pathological conditions can be
CC diagnosed by determining the amount of the new polypeptides in a sample

```
CC   or by determining the presence of mutations in the new genes. Specific
CC   uses are described for each of the 97 genes, based on which tissues they
CC   are most highly expressed in, and include developing products for the
CC   diagnosis or treatment of cancer, tumours, developmental abnormalities
CC   and foetal deficiencies, blood disorders, diseases of the immune system,
CC   autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive
CC   disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin
CC   disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney
CC   disorders, digestive/endocrine disorders, infections and AIDS. The
CC   polypeptides are also useful for identifying their binding partners.
CC   The sequences shown in AAY76224 to AAY76424 represent fragments of the
CC   secreted proteins.
XX
SQ   Sequence   389 AA;


  Query Match             99.6%;  Score 2003;  DB 21;  Length 389;
  Best Local Similarity   99.7%;  Pred. No. 2.7e-142;
  Matches  388;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps
0;

Qy       1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mislpgplvtnllrflflglsalappsraqlqlhlpanrlqaveggevvlpawytlhgev 60

Qy      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sssqpwevpfvmwffkqkekedqvlsyingvttskpgvslvysmpsrnlslrleglqekd 120

Qy     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
           ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 sgpyscsvnvqnkqgksrghsiktlelnvlvppappscrlqgvphvganvtlscqsprsk 180

Qy     181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 pavqyqwdrqlpsfqtffapaldvirgslsltnlsssmagvyvckahnevgtaqcnvtle 240

Qy     241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 vstgpgaavvagavvgtlvglgllaglvllyhrrgkaleepandikedaiaprtlpwpks 300

Qy     301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 sdtiskngtlssvtsaralrpphgpprpgaltptpslssqalpsprlpttdgahpqpisp 360

Qy     361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSL 389
           |||||||||||||||||||||||||||||
Db     361 ipggvsssglsrmgavpvmvpaqsqagsl 389


RESULT  15
AAB65832
ID   AAB65832 standard; Protein; 370 AA.
XX
AC   AAB65832;
XX
DT   28-MAR-2001  (first entry)
XX
DE   Human INTERCEPT 258 SEQ ID NO: 28.
XX
KW   Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;
KW   INTERCEPT 258; coronary disorder; olfactory disorder;
KW   neurological disorder; pulmonary disorder; immunological disorder;
KW   developmental disorder; kidney disorder.
XX
OS   Homo sapiens.
XX
PN   WO200078808-A1.
XX
PD   28-DEC-2000.
XX
PF   19-JUN-2000; 2000WO-US16883.
XX
PR   18-JUN-1999;   99US-0336536.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Leiby KR,  McKay C,  Bossone S;
XX
DR   WPI; 2001-050109/06.
XX
PT   New nucleic acids for treating diseases and disorders, e.g.
PT   atherosclerosis, infection, autoimmune diseases, obesity, ear
PT   disorders, brain disorders, tumors, diabetes, arthritis, multiple
PT   sclerosis and asthma -
XX
PS   Claim 9; Page 228-229; 332pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC    human and murine secreted or transmembrane proteins TANGO 253, TANGO
257,
CC   TANGO 281 and INTERCEPT 258. These are useful in the treatment of
CC   coronary, pulmonary, olfactory, immunological, neurological,
CC   developmental and kidney disorders.
XX
SQ   Sequence   370 AA;


  Query Match             86.4%;  Score 1738.5;  DB 22;  Length 370;
  Best Local Similarity   94.2%;  Pred. No. 1.8e-122;
  Matches  341;  Conservative    3;  Mismatches   11;  Indels    7;  Gaps
1;

Qy       1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
           |||||||||||| |||||||||||||||||||||||||||| ||    |||||| ||
Db       1 mislpgplvtnlxrflflglsalappsraqlqlhlpanrlqaveegesgasawytlhrev 60

Qy      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db      61 sssqpwevpfvmwffkqkekedqvlsyingvttskpgvslvysmpsrnlslrveglqekd 120

Qy     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 sgpyscsvnvqdkqgksrghsiktlelnvlvppappscrlqgvphvganvtlscqsprsk 180

Qy     181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 pavqyqwdrqlpsfqtffapaldvirgslsltnlsssmagvyvckahnevgtaqcnvtle 240

Qy    241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 vstgpgaavvaeavvgtlvglgllaglvllyhrrgkaleepandikedaiaprtlpwpks 300

Qy    301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPR-------LPTTDGA 353
          ||||||||||||||||||||||||||||||||||||||||||||||        |:|:
Db    301 sdtiskngtlssvtsaralrpphgpprpgaltptpslssqalpsprhahdrwgppstnip 360

Qy    354 HP 355
          ||
Db    361 hp 362



Search completed: August 19, 2002, 17:09:06
Job time: 3349 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 16:16:12 ; Search time 24.02 Seconds
(without alignments)
396.585 Million cell updates/sec

Title: US-09-902-759-39
Perfect score: 2012
Sequence: 1 MISLPGPLVTNLLRFLFLGL.....SRMGAVPVMVPAQSQAGSLV 390

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2012	100.0	390	2	US-08-979-424-1	Sequence 1, Appli
2	353.5	17.6	365	4	US-08-928-383B-26	Sequence 26, Appl
3	346	17.2	365	4	US-08-928-383B-2	Sequence 2, Appli
4	345.5	17.2	365	4	US-08-928-383B-23	Sequence 23, Appl
5	343	17.0	365	2	US-08-979-424-3	Sequence 3, Appli
6	343	17.0	365	4	US-09-272-496-2	Sequence 2, Appli
7	297	14.8	319	1	US-08-597-495B-22	Sequence 22, Appl
8	297	14.8	319	4	US-09-068-051A-22	Sequence 22, Appl
9	290.5	14.4	365	4	US-08-928-383B-24	Sequence 24, Appl
10	289.5	14.4	387	4	US-09-175-928-2	Sequence 2, Appli
11	258	12.8	318	4	US-09-068-051A-32	Sequence 32, Appl
12	176	8.7	299	4	US-09-188-930-331	Sequence 331, App
13	176	8.7	299	4	US-09-462-270-2	Sequence 2, Appli
14	171	8.5	299	4	US-09-188-930-189	Sequence 189, App
15	158.5	7.9	501	2	US-08-408-095-31	Sequence 31, Appl
16	153.5	7.6	344	2	US-08-602-725-34	Sequence 34, Appl
17	152	7.6	1101	3	US-08-986-485-2	Sequence 2, Appli
18	134	6.7	607	2	US-08-752-307B-12	Sequence 12, Appl
19	133	6.6	321	6	5169835-17	Patent No. 5169835
20	133	6.6	464	2	US-08-602-725-32	Sequence 32, Appl
21	133	6.6	642	1	US-08-217-299-1	Sequence 1, Appli
22	133	6.6	698	2	US-08-602-725-36	Sequence 36, Appl
23	133	6.6	734	2	US-08-389-459A-17	Sequence 17, Appl
24	133	6.6	734	3	US-08-987-867A-17	Sequence 17, Appl
25	132.5	6.6	252	2	US-08-414-657D-56	Sequence 56, Appl
26	132.5	6.6	287	2	US-08-414-657D-48	Sequence 48, Appl
27	132.5	6.6	304	2	US-08-414-657D-44	Sequence 44, Appl
28	132.5	6.6	308	2	US-08-414-657D-46	Sequence 46, Appl
29	132.5	6.6	325	2	US-08-414-657D-2	Sequence 2, Appli
30	132.5	6.6	325	2	US-08-414-657D-41	Sequence 41, Appl
31	132.5	6.6	338	2	US-08-414-657D-60	Sequence 60, Appl
32	132.5	6.6	1241	4	US-09-040-774-2	Sequence 2, Appli
33	132	6.6	828	1	US-08-261-304-2	Sequence 2, Appli
34	130	6.5	1091	3	US-08-986-485-5	Sequence 5, Appli
35	129	6.4	917	1	US-08-245-295-2	Sequence 2, Appli
36	129	6.4	917	1	US-08-481-130-2	Sequence 2, Appli
37	129	6.4	917	1	US-08-656-984A-2	Sequence 2, Appli
38	129	6.4	917	1	US-08-485-604-2	Sequence 2, Appli
39	129	6.4	917	2	US-08-487-595-2	Sequence 2, Appli
40	128.5	6.4	252	2	US-08-414-657D-57	Sequence 57, Appl
41	128.5	6.4	287	2	US-08-414-657D-49	Sequence 49, Appl
42	128.5	6.4	310	2	US-08-414-657D-45	Sequence 45, Appl
43	128.5	6.4	315	2	US-08-414-657D-47	Sequence 47, Appl
44	128.5	6.4	338	2	US-08-414-657D-42	Sequence 42, Appl
45	128.5	6.4	338	2	US-08-414-657D-43	Sequence 43, Appl

ALIGNMENTS

```
RESULT 1
US-08-979-424-1
; Sequence 1, Application US/08979424
; Patent No. 5942606
; GENERAL INFORMATION:
;   APPLICANT: Lal, Preeti
;   APPLICANT: Corley, Neil C.
;   TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN
;   NUMBER OF SEQUENCES: 3
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Incyte Pharmaceuticals, Inc.
;     STREET: 3174 Porter Dr.
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
```

```
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/979,424
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0405 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  390 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  LUNGFET03
;      CLONE:  1232054
US-08-979-424-1


  Query Match             100.0%;  Score 2012;  DB 2;  Length 390;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-168;
  Matches  390;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60

Qy     61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120

Qy    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180

Qy    181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240

Qy    241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300

Qy    301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
```

```
Qy    361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
          ||||||||||||||||||||||||||||||
Db    361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390


RESULT   2
US-08-928-383B-26
; Sequence 26, Application US/08928383B
; Patent No. 6210921
;  GENERAL INFORMATION:
;    APPLICANT:  Robert W. Finberg, Jeffrey M. Bergelson,
;    APPLICANT:  and Marshall S. Horwitz
;    TITLE OF INVENTION:  CAR, A No. 6210921el Coxsackievirus and Adenovirus
;    TITLE OF INVENTION:  Receptor
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/928,383B
;      FILING DATE:  12-SEP-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/026,100
;      FILING DATE:  13-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mandragouras, Amy E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  DFN-020
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  365 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-928-383B-26


  Query Match             17.6%;  Score 353.5;  DB 4;  Length 365;
  Best Local Similarity   27.8%;  Pred. No. 4.7e-23;
  Matches  113;  Conservative   71;  Mismatches  156;  Indels   67;  Gaps
15;

Qy      9 VTNLLRFLFL-GLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSSSQPWE 67
          :  || |: | |::       : | :  |  |::  :|    ||  :||  |     | :
Db      1 MARLLCFVLLCGIADFT----SGLSITTPEQRIEKAKGETAYLPCKFTLSPE--DQGPLD 54
```

```
Qy      68 VPFVMWFFKQKEKE--DQVLSYINGVTTSKPGVSLVY---------------SMPSRNL 109
           :    |     : :  |||:   :|          :|                 : | :
Db      55 IE---WLISPSDNQIVDQVIILYSG--------DKIYDNYYPDLKGRVHFTSNDVKSGDA 103

Qy     110 SLRLEGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGAN 169
           |: :  ||  | | | | |       |: | : |   | ||| |:   | : |   :| :
Db     104 SINVTNLQLSDIGTYQCKVK------KAPGVANKKFLLTVLVKPSGTRCFVDGSEEIGND 157

Qy     170 VTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPAL-DVIRGSLSLTNLSSSMAGVYVCKAHN 228
             | |:       :|::| ::|   ||   | | ::    :|: | ||  :| | |   |
Db     158 FKLKCEPKEGSLPLQFEW-QKLSDSQTMPTPWLAEMTSPVISVKNASSEYSGTYSCTVQN 216

Qy     229 EVGTAQCNVTLE-VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRR---GKALEEPAND 284
           ||: || : |: |     |  :||||:|||: | |:  ::   ||:    |  :|  :|
Db     217 RVGSDQCMLRLDVVPPSNRAGTIAGAVIGTLLALVLIGAILFCCHRKRREEKYEKEVHHD 276

Qy     285 IKEDAIAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPS 344
           |:||      :| |||  : :::   |: :|             |:::|:
Db     277 IRED------VPPPKSRTSTARSYIGSNHSSL-----------GSMSPSNMEGYSKTQY 318

Qy     345 PRLPTTDGAH-PQPISPIPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
           ::|: |    ||  :  |  |::  ||||||||||:||||: ||:|
Db     319 NQVPSEDFERAPQSPTLAPAKVAAPNLSRMGAVPVMIPAQSKDGSIV 365
```

Search completed: August 19, 2002, 17:09:51
Job time: 3219 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 16:21:32 ; Search time 42.75 Seconds
(without alignments)
876.604 Million cell updates/sec

Title: US-09-902-759-39
Perfect score: 2012
Sequence: 1 MISLPGPLVTNLLRFLFLGL.....SRMGAVPVMVPAQSQAGSLV 390

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	176	8.7	299	2	S56749	junctional adhesio
2	162.5	8.1	344	2	A27681	nonspecific cross-
3	158.5	7.9	847	2	JH0371	B-cell adhesion pr
4	155.5	7.7	3707	2	S18252	heparan sulfate pr
5	154.5	7.7	4391	2	A38096	perlecan precursor
6	153.5	7.6	647	2	A35648	B-cell adhesion pr
7	153.5	7.6	1040	2	A49356	transient axonal g
8	152.5	7.6	521	2	S34338	biliary glycoprote
9	152	7.6	483	2	T17346	hypothetical prote
10	151.5	7.5	1036	2	S22383	axonin 1 precursor
11	151.5	7.5	4162	2	T42633	connectin/titin -
12	150.5	7.5	521	2	JC1508	biliary glycoprote
13	150.5	7.5	1040	2	A34695	axonal glycoprotei
14	150	7.5	868	2	A46512	CD22 homolog/B lym
15	149.5	7.4	341	2	JC1512	biliary glycoprote
16	147	7.3	5175	2	T20992	hypothetical prote
17	147	7.3	5198	2	T43290	hemicentin precurs
18	144	7.2	349	2	A34815	carcinoembryonic a
19	143	7.1	862	2	I49583	differentiation an
20	142	7.1	278	2	A39037	carcinoembryonic a
21	141.5	7.0	26926	1	I38344	titin, cardiac mus
22	141	7.0	458	2	JC1509	biliary glycoprote
23	139	6.9	458	1	WMMSR1	biliary glycoprote
24	138.5	6.9	495	2	A55181	pregnancy-specific
25	138.5	6.9	1323	2	PN0568	connectin 3B - chi
26	138	6.9	278	2	JC1506	biliary glycoprote
27	138	6.9	419	2	B54312	pregnancy-specific
28	137	6.8	7962	2	I38346	elastic titin - hu
29	136.5	6.8	518	2	JC4024	poliovirus recepto
30	135.5	6.7	426	2	C55181	pregnancy-specific
31	135.5	6.7	426	2	B35334	pregnancy-specific
32	135	6.7	428	2	JS0032	pregnancy-specific
33	135	6.7	428	2	I57486	pregnancy-specific
34	134	6.7	240	2	JC4121	pregnancy-specific
35	134	6.7	436	2	B55181	pregnancy-specific
36	133	6.6	321	2	JH0395	biliary glycoprote
37	133	6.6	351	2	JH0396	biliary glycoprote
38	133	6.6	417	2	JH0394	biliary glycoprote
39	133	6.6	419	2	A36109	pregnancy-specific
40	133	6.6	464	2	C30127	transmembrane carc
41	133	6.6	526	1	A32164	biliary glycoprote
42	133	6.6	702	2	A36319	carcinoembryonic a
43	132.5	6.6	166	2	A33402	pregnancy-specific
44	132.5	6.6	338	2	JC4776	limbic-system-asso
45	132.5	6.6	338	2	JC1238	opioid-binding pro

ALIGNMENTS

RESULT 1
S56749
junctional adhesion molecule precursor - human
N;Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet F11 receptor
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: A59406; S56749
R;Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; Kita, T.
J. Immunol. 163, 553-557, 1999
A;Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribution of junctional adhesion molecule in human endothelial cells.
A;Reference number: A59406; MUID:99323940; PMID:10395639
A;Accession: A59406
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-299 <OZA>
A;Cross-references: GB:AAD42050; NID:g5326797; PIDN:AAD42050.1
R;Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.
Biochem. J. 310, 155-162, 1995
A;Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of a novel platelet receptor for monoclonal antibody F11 with the Fc-gamma-RII receptor.
A;Reference number: S56749; MUID:95374438; PMID:7646439
A;Accession: S56749
A;Molecule type: protein
A;Residues: 28-49,'X',51-53;62-73,'E',75-103;123,'F',125-130;'FDKDXTIYLNXY';'LT',206,'X',208,'Q' <NAI>
A;Note: the order of the peptides other than the amino terminus was not determined
C;Genetics:
A;Gene: JAM
C;Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-299/Product: junctional adhesion molecule #status predicted <MAT>

Query Match 8.7%; Score 176; DB 2; Length 299;
Best Local Similarity 25.7%; Pred. No. 0.00014;
Matches 71; Conservative 46; Mismatches 129; Indels 30; Gaps 12;

```
Qy       9 VTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSSSQPWEV 68
Db       7 VERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYS---------GFSS 57

Qy      69 PFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPYSCSV 128
Db      58 PRVEWKFDQGD-TTRLVCYNNKITASYE--DRVTFLPT---GITFKSVTREDTGTYTCMV 111

Qy     129 NVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQWD 188
Db     112 S--EEGGNSYG-EVK-VKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWF 167

Qy     189 RQ---LP----SFQTF--FAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQ-CNVT 238
Db     168 KDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAV 227

Qy     239 LEVSTGPGAAVVAGAVVGTLVGLGLLA-GLVLLYHR 273
Db     228 RMEAVERNVGVIVAAVLVTLILLGILVFGIWFAYSR 263
```

Search completed: August 19, 2002, 17:10:57
Job time: 2965 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 17:11:02 ; Search time 24.06 Seconds
(without alignments)
627.624 Million cell updates/sec

Title: US-09-902-759-39
Perfect score: 2012
Sequence: 1 MISLPGPLVTNLLRFLFLGL.....SRMGAVPVMVPAQSQAGSLV 390

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	353.5	17.6	365	1	CXAR_MOUSE	P97792 mus musculu
2	343	17.0	365	1	CXAR_HUMAN	P78310 homo sapien
3	297	14.8	319	1	A33_HUMAN	Q99795 homo sapien
4	212	10.5	298	1	JAM2_HUMAN	P57087 homo sapien
5	176	8.7	299	1	JAM1_HUMAN	Q9y624 homo sapien
6	168.5	8.4	300	1	JAM1_MOUSE	O88792 mus musculu
7	167.5	8.3	298	1	JAM1_BOVIN	Q9xt56 bos taurus
8	163	8.1	344	1	CEA6_HUMAN	P40199 homo sapien
9	158.5	7.9	4393	1	PGBM_HUMAN	P98160 homo sapien
10	155.5	7.7	3707	1	PGBM_MOUSE	Q05793 mus musculu
11	153.5	7.6	847	1	CD22_HUMAN	P20273 homo sapien
12	153.5	7.6	1040	1	AXO1_HUMAN	Q02246 homo sapien
13	151.5	7.5	1036	1	AXO1_CHICK	P28685 gallus gall
14	150.5	7.5	521	1	CEA1_MOUSE	P31809 mus musculu
15	150.5	7.5	1040	1	AXO1_RAT	P22063 rattus norv
16	146	7.3	515	1	PVR1_PIG	Q9gl76 sus scrofa
17	145	7.2	517	1	PVR1_HUMAN	Q15223 homo sapien
18	144	7.2	349	1	CEA8_HUMAN	P31997 homo sapien
19	143	7.1	862	1	CD22_MOUSE	P35329 mus musculu
20	142.5	7.1	1709	1	SN_HUMAN	Q9bzz2 homo sapien
21	138.5	6.9	515	1	PVR1_MOUSE	Q9jkf6 mus musculu
22	138	6.9	348	1	KILO_RAT	Q9z0j8 rattus norv
23	138	6.9	419	1	PSG4_HUMAN	Q00888 homo sapien
24	135.5	6.7	426	1	PSGB_HUMAN	Q00887 homo sapien
25	135	6.7	428	1	PSG3_HUMAN	Q16557 homo sapien
26	134.5	6.7	337	1	G55A_CHICK	Q98892 gallus gall
27	133	6.6	526	1	CEA1_HUMAN	P13688 homo sapien
28	133	6.6	702	1	CEA5_HUMAN	P06731 homo sapien
29	132.5	6.6	338	1	LAMP_HUMAN	Q13449 homo sapien
30	132.5	6.6	345	1	OPCM_HUMAN	Q14982 homo sapien
31	132.5	6.6	345	1	OPCM_RAT	P32736 rattus norv
32	132	6.6	252	1	CEA3_HUMAN	P40198 homo sapien
33	131.5	6.5	349	1	LACH_SCHAM	Q26474 schistocerc
34	131.5	6.5	538	1	PVR2_HUMAN	Q92692 homo sapien
35	131	6.5	519	1	ECTO_RAT	P16573 rattus norv
36	130.5	6.5	837	1	NCM2_MOUSE	O35136 mus musculu
37	130	6.5	761	1	NCA2_HUMAN	P13592 homo sapien
38	130	6.5	917	1	ICA5_MOUSE	Q60625 mus musculu
39	129.5	6.4	345	1	OPCM_BOVIN	P11834 bos taurus
40	128.5	6.4	338	1	LAMP_RAT	Q62813 rattus norv
41	128.5	6.4	837	1	NCM2_HUMAN	O15394 homo sapien
42	128	6.4	338	1	LAMP_CHICK	Q98919 gallus gall
43	128	6.4	530	1	PVR2_MOUSE	P32507 mus musculu
44	126.5	6.3	404	1	RAGE_HUMAN	Q15109 homo sapien
45	126	6.3	335	1	PSG5_HUMAN	Q15238 homo sapien

ALIGNMENTS

RESULT 1
CXAR_MOUSE
ID CXAR_MOUSE STANDARD; PRT; 365 AA.
AC P97792; O09052;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Coxsackievirus and adenovirus receptor homolog precursor (mCAR).
GN CXADR OR CAR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=97190109; PubMed=9036860;
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT "Isolation of a common receptor for Coxsackie B viruses and
RT adenoviruses 2 and 5.";
RL Science 275:1320-1323(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/MAI;

```
RX   MEDLINE=97250541; PubMed=9096397;
RA   Tomko R.P., Xu R., Philipson L.;
RT   "HCAR and MCAR: the human and mouse cellular receptors for subgroup C
RT   adenoviruses and group B coxsackieviruses.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RA   Bergelson J.M., Krithivas A., Crowell T.L., Finberg R.W.;
RT   "The murine CAR homologue (mCAR) is a receptor for coxsackie B
RT   viruses and adenoviruses.";
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
C                                       C
---------------------------------------------------------------------------
CC      This SWISS-PROT entry is copyright. It is produced through a
collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation
-
CC   the European Bioinformatics Institute. There are no restrictions on
its
CC   use by non-profit institutions as long as its content is in no
way
CC    modified and this statement is not removed. Usage by and for
commercial
C C        entities requires a license agreement (See
http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
C                                       C
---------------------------------------------------------------------------
DR   EMBL; Y10320; CAA71368.1; -.
DR   EMBL; U90715; AAC53148.1; -.
DR   EMBL; Y11929; CAA72679.1; -.
DR   MGD; MGI:1201679; Cxadr.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00408; IGc2; 1.
KW   Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Repeat.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    365       COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR
FT                                 HOMOLOG.
FT   DOMAIN       20    237       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    238    258       POTENTIAL.
FT   DOMAIN      259    365       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       34    127       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN      155    219       IG-LIKE C2-TYPE DOMAIN 2.
FT   DISULFID     41    120       BY SIMILARITY.
FT   DISULFID    162    212       BY SIMILARITY.
FT   CARBOHYD    106    106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    201    201       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    340    365       VAAPNLSRMGAVPVMIPAQSKDGSIV -> FKYAYKTDGIT
FT                                 VV (IN REF. 2 AND 3).
```

```
SQ   SEQUENCE   365 AA;  39947 MW;  5445B4B52A34B2A2 CRC64;


  Query Match             17.6%;  Score 353.5;  DB 1;  Length 365;
  Best Local Similarity   27.8%;  Pred. No. 1.8e-16;
  Matches  113;  Conservative   71;  Mismatches  156;  Indels   67;  Gaps
15;

Qy       9 VTNLLRFLFL-GLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSSSQPWE 67
           :  || |: | |::       : | :  |  |::  :|    ||  :||  |     | :
Db       1 MARLLCFVLLCGIADFT----SGLSITTPEQRIEKAKGETAYLPCKFTLSPE--DQGPLD 54

Qy      68 VPFVMWFFKQKEKE--DQVLSYINGVTTSKPGVSLVY---------------SMPSRNL 109
           :    |     : :  |||:   :|          :|                 : | :
Db      55 IE---WLISPSDNQIVDQVIILYSG--------DKIYDNYYPDLKGRVHFTSNDVKSGDA 103

Qy     110 SLRLEGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGAN 169
           |: :  ||  | | | | |       |: | : |   | ||| |:   | : |   :| :
Db     104 SINVTNLQLSDIGTYQCKVK------KAPGVANKKFLLTVLVKPSGTRCFVDGSEEIGND 157

Qy     170 VTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPAL-DVIRGSLSLTNLSSSMAGVYVCKAHN 228
           | |:       :|::| ::|   ||   | | ::    :|: | ||  :| | |   |
Db     158 FKLKCEPKEGSLPLQFEW-QKLSDSQTMPTPWLAEMTSPVISVKNASSEYSGTYSCTVQN 216

Qy     229 EVGTAQCNVTLE-VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRR---GKALEEPAND 284
           ||: || : |: |      | :||||:|||: | |:  ::   ||:    | :| :|
Db     217 RVGSDQCMLRLDVVPPSNRAGTIAGAVIGTLLALVLIGAILFCCHRKRREEKYEKEVHHD 276

Qy     285 IKEDAIAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPS 344
           |:||      :| |||  : :::   |: :|             |:::|:
Db     277 IRED------VPPPKSRTSTARSYIGSNHSSL-----------GSMSPSNMEGYSKTQY 318

Qy     345 PRLPTTDGAH-PQPISPIPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
           ::|: |    ||  :  |  |::  ||||||||||:||||: ||:|
Db     319 NQVPSEDFERAPQSPTLAPAKVAAPNLSRMGAVPVMIPAQSKDGSIV 365


Search completed: August 19, 2002, 17:18:28
Job time: 446 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 17:09:12 ; Search time 67.26 Seconds
(without alignments)
1003.093 Million cell updates/sec

Title: US-09-902-759-39
Perfect score: 2012
Sequence: 1 MISLPGPLVTNLLRFLFLGL.....SRMGAVPVMVPAQSQAGSLV 390

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2012	100.0	390	4	Q96AP7	Q96ap7 homo sapien
2	2009	99.9	390	4	Q96T50	Q96t50 homo sapien
3	1931	96.0	390	6	Q95KI3	Q95ki3 macaca fasc
4	1397	69.4	394	11	Q925F2	Q925f2 mus musculu
5	641.5	31.9	204	11	Q9D7I2	Q9d7i2 mus musculu
6	343	17.0	366	11	Q9DBJ8	Q9dbj8 mus musculu
7	341.5	17.0	372	13	Q90Y50	Q90y50 brachydanio
8	330	16.4	358	11	Q9R066	Q9r066 rattus norv
9	324.5	16.1	327	4	Q96IQ7	Q96iq7 homo sapien
10	320.5	15.9	325	4	O95791	O95791 homo sapien
11	316	15.7	407	11	Q9D2J4	Q9d2j4 mus musculu
12	307.5	15.3	373	4	Q9H6B4	Q9h6b4 homo sapien
13	290	14.4	284	4	Q9NX42	Q9nx42 homo sapien
14	287	14.3	373	11	Q920S5	Q920s5 mus musculu
15	279.5	13.9	318	13	Q91664	Q91664 xenopus lae
16	277.5	13.8	300	11	Q9D9J0	Q9d9j0 mus musculu
17	276.5	13.7	300	11	Q9DA22	Q9da22 mus musculu
18	272	13.5	352	11	Q91W66	Q91w66 mus musculu
19	269	13.4	304	11	Q9CVA4	Q9cva4 mus musculu
20	267.5	13.3	328	11	Q9Z109	Q9z109 mus musculu
21	267.5	13.3	344	11	Q9R067	Q9r067 rattus norv
22	266	13.2	335	13	Q9PWR4	Q9pwr4 gallus gall
23	264.5	13.1	344	4	Q9UKV4	Q9ukv4 homo sapien
24	263	13.1	335	13	Q9YGH1	Q9ygh1 gallus gall
25	262.5	13.0	259	4	O95532	O95532 homo sapien
26	259	12.9	319	11	Q922D5	Q922d5 mus musculu
27	258	12.8	319	6	Q9TU80	Q9tu80 canis famil
28	258	12.8	319	11	Q9JKA5	Q9jka5 mus musculu
29	257	12.8	248	11	Q9D0T4	Q9d0t4 mus musculu
30	256	12.7	319	6	Q9TU79	Q9tu79 sus scrofa
31	253	12.6	335	13	Q9YGV5	Q9ygv5 gallus gall
32	221	11.0	181	13	Q91665	Q91665 xenopus lae
33	196	9.7	577	11	Q9D2Z1	Q9d2z1 mus musculu
34	186.5	9.3	977	4	Q96RD9	Q96rd9 homo sapien
35	183	9.1	300	11	Q9JHY1	Q9jhy1 rattus norv
36	176	8.7	298	11	Q9JI59	Q9ji59 mus musculu
37	171	8.5	381	4	Q9Y4A4	Q9y4a4 homo sapien
38	169.5	8.4	309	4	Q96FL1	Q96fl1 homo sapien
39	169.5	8.4	310	4	Q9BX67	Q9bx67 homo sapien
40	168.5	8.4	430	4	Q15600	Q15600 homo sapien
41	166.5	8.3	310	11	Q9D8B7	Q9d8b7 mus musculu
42	166	8.3	310	11	Q9EPK4	Q9epk4 mus musculu
43	166	8.3	310	11	Q9D1M9	Q9d1m9 mus musculu
44	164	8.2	538	4	Q9NWQ7	Q9nwq7 homo sapien
45	163.5	8.1	512	4	Q96DN8	Q96dn8 homo sapien

ALIGNMENTS

RESULT 1
Q96AP7
ID Q96AP7 PRELIMINARY; PRT; 390 AA.
AC Q96AP7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 41.2 KDA PROTEIN.

```
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON ADENOCARCINOMA;
RA   Strausberg R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC016868; AAH16868.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   390 AA;  41176 MW;  C5E3F302F41B6EEC CRC64;


  Query Match             100.0%;  Score 2012;  DB 4;  Length 390;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-156;
  Matches  390;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy       1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60

Qy      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120

Qy     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180

Qy     181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240

Qy     241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300

Qy     301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360

Qy     361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
           ||||||||||||||||||||||||||||||
Db     361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390


RESULT   2
Q96T50
ID   Q96T50      PRELIMINARY;      PRT;   390 AA.
AC   Q96T50;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ENDOTHELIAL CELL-SELECTIVE ADHESION MOLECULE.
GN   ESAM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21238298; PubMed=11279107;
RA   Hirata K.-I., Ishida T., Penta K., Rezaee M., Yang E., Wohlgemuth J.,
RA   Quertermous T.;
RT   "Cloning of an immunoglobulin family adhesion molecule selectively
RT   expressed by endothelial cells.";
RL   J. Biol. Chem. 276:16223-16231(2001).
DR   EMBL; AF361746; AAK51065.1; -.
SQ   SEQUENCE   390 AA;  41208 MW;  C5E3EEB5F41B6EEC CRC64;


  Query Match             99.9%;  Score 2009;  DB 4;  Length 390;
  Best Local Similarity   99.7%;  Pred. No. 1.7e-155;
  Matches  389;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps
0;

Qy       1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60

Qy      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120

Qy     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180

Qy     181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240

Qy     241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300

Qy     301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360

Qy     361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
           |||||||||||||||||||:||||||||||
Db     361 IPGGVSSSGLSRMGAVPVMMPAQSQAGSLV 390


RESULT   3
Q95KI3
ID   Q95KI3      PRELIMINARY;      PRT;   390 AA.
AC   Q95KI3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 40.9 KDA PROTEIN.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TEMPORAL LOBE RIGHT;
RA   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA   Suzuki Y., Sugano S., Hashimoto K.;
RT   "Isolation of full-length cDNA clones from macaque brain cDNA
RT   libraries.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB060855; BAB46874.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   390 AA;  40946 MW;  CDBF63F2BD464EF5 CRC64;


  Query Match             96.0%;  Score 1931;  DB 6;  Length 390;
  Best Local Similarity   96.4%;  Pred. No. 3.8e-149;
  Matches  376;  Conservative    6;  Mismatches    8;  Indels    0;  Gaps
0;

Qy       1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV 60
           |||||||||||||||||||||||||||||:|||||||:||||||||||||||||||| ||
Db       1 MISLPGPLVTNLLRFLFLGLSALAPPSRAELQLHLPANQLQAVEGGEVVLPAWYTLHAEV 60

Qy      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120
           ||:|| |||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      61 SSAQPGEVPFVMWFFKDKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD 120

Qy     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK 180
           |||||||||||| |:: |||||||||||||||||||||||| ||||||||||||||||||
Db     121 SGPYSCSVNVQDKNGQASGHSIKTLELNVLVPPAPPSCRLQGVPRVGANVTLSCQSPRSK 180

Qy     181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     181 PAVQYQWDRQLPSFQTFFAPVLDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE 240

Qy     241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS 300

Qy     301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db     301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGANPQPISL 360

Qy     361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
           ||||||||||||||||||||||||||||||
Db     361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390


RESULT   4
Q925F2
ID   Q925F2      PRELIMINARY;      PRT;   394 AA.
AC   Q925F2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ENDOTHELIAL CELL-SELECTIVE ADHESION MOLECULE.
GN   ESAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SWISS WEBSTER/NIH;
RX   MEDLINE=21238298; PubMed=11279107;
RA   Hirata K.-I., Ishida T., Penta K., Rezaee M., Yang E., Wohlgemuth J.,
RA   Quertermous T.;
RT   "Cloning of an immunoglobulin family adhesion molecule selectively
RT   expressed by endothelial cells.";
RL   J. Biol. Chem. 276:16223-16231(2001).
DR   EMBL; AF361882; AAK51504.1; -.
SQ   SEQUENCE   394 AA;  41810 MW;  3D2B354943A2227D CRC64;


  Query Match             69.4%;  Score 1397;  DB 11;  Length 394;
  Best Local Similarity   72.3%;  Pred. No. 1.1e-105;
  Matches  285;  Conservative   33;  Mismatches   72;  Indels    4;  Gaps
3;

Qy       1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLP--ANRLQAVEGGEVVLPAWYTLHG 58
           ||   |   |:||| |||||| ||  ||||::||:|   |:|:|||| |||||||||:
Db       1 MILQAGTPETSLLRVLFLGLSTLAAFSRAQMELHVPPGLNKLEAVEGEEVVLPAWYTMAR 60

Qy      59 EVSSSQPWEVPFVMWFFKQKEKE-DQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQ 117
           | | | | ||| ::|| :|: || :|||||||| |:||| :||:|: |||:|||| ||
Db      61 EESWSHPREVPILIWFLEQEGKEPNQVLSYINGVMTNKPGTALVHSISSRNVSLRLGALQ 120

Qy     118 EKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSP 177
           | ||| | ||||||: :||| |||||::|| |||||||||| |||||:|| ||||:|:||
Db     121 EGDSGTYRCSVNVQNDEGKSIGHSIKSIELKVLVPPAPPSCSLQGVPYVGTNVTLNCKSP 180

Qy     178 RSKPAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNV 237
           ||||  ||||:|  || | || |||| :|||| ||||| :|:||||||| | || |:|||
Db     181 RSKPTAQYQWERLAPSSQVFFGPALDAVRGSLKLTNLSIAMSGVYVCKAQNRVGFAKCNV 240

Qy     238 TLEVSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPW 297
           ||:| ||  |||||||||||| ||| |:||||||| || | ||| ||||||||||||||||
Db     241 TLDVMTGSKAAVVAGAVVGTFVGLVLIAGLVLLYQRRSKTLEELANDIKEDAIAPRTLPW 300

Qy     298 PKSSDTISKNGTLSSVTSARALRPPH-GPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQ 356
           | |||||||||||||||||||||||   ||||| |||||:||||| |||||  |   ||
Db     301 TKGSDTISKNGTLSSVTSARALRPPKAAPPRPGTFTPTPSVSSQALSSPRLPRVDEPPPQ 360

Qy     357 PISPIPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
           :|  ||||||| ||||||||||||||||||||||
Db     361 AVSLTPGGVSSSALSRMGAVPVMVPAQSQAGSLV 394


RESULT   5
Q9D7I2
ID   Q9D7I2      PRELIMINARY;      PRT;   204 AA.
AC   Q9D7I2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
```

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 2310008D05RIK PROTEIN.
GN ESAM OR 2310008D05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK009223; BAB26146.1; -.
DR MGD; MGI:1916774; Esam.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_like; 1.
SQ SEQUENCE 204 AA; 22352 MW; 021B29BE2B05F494 CRC64;

Query Match 31.9%; Score 641.5; DB 11; Length 204;
Best Local Similarity 66.2%; Pred. No. 1.5e-44;
Matches 129; Conservative 25; Mismatches 38; Indels 3; Gaps 2;

```
Qy       1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLP--ANRLQAVEGGEVVLPAWYTLHG 58
           ||   |   |:||| |||||| ||  ||||::||:|   |:|:|||| |||||||||:
Db       1 MILQAGTPETSLLRVLFLGLSTLAAFSRAQMELHVPPGLNKLEAVEGEEVVLPAWYTMAR 60

Qy      59 EVSSSQPWEVPFVMWFFKQKEKE-DQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQ 117
           | | | | ||| ::|| :|: || :||||||||| |:||| :||:|: |||:|||| ||
Db      61 EESWSHPREVPILIWFLEQEGKEPNQVLSYINGVMTNKPGTALVHSISSRNVSLRLGALQ 120

Qy     118 EKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSP 177
           | ||| | ||||||: :||| |||||::|| |||||||||| |||||:|| ||||:|:||
Db     121 EGDSGTYRCSVNVQNDEGKSIGHSIKSIELKVLVPPAPPSCSLQGVPYVGTNVTLNCKSP 180

Qy     178 RSKPAVQYQWDRQLP 192
           ||||  ||||:|  |
Db     181 RSKPTAQYQWERLAP 195
```

Search completed: August 19, 2002, 17:15:52
Job time: 400 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 15:01:07 ; Search time 2294.29 Seconds
(without alignments)
16536.624 Million cell updates/sec

Title: US-09-902-759-38
Perfect score: 1813
Sequence: 1 ggagccgccctgggtgtcag.....cataatgtttgtatgaaaaa 1813

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1813	100.0	1813	6	AX076924	AX076924 Sequence
	2	1809.8	99.8	1838	9	AF361746	AF361746 Homo sapi
	3	1809	99.8	1821	6	AX136161	AX136161 Sequence
	4	1804.8	99.5	1816	6	AX191598	AX191598 Sequence
	5	1760.4	97.1	1831	6	AX073678	AX073678 Sequence
	6	1691.8	93.3	1734	9	BC016868	BC016868 Homo sapi
	7	1659.6	91.5	1855	9	AB060855	AB060855 Macaca fa
	8	1171.4	64.6	1173	6	AX191588	AX191588 Sequence
	9	861.6	47.5	1840	10	AF361882	AF361882 Mus muscu
c	10	828.2	45.7	187960	9	AP000866	AP000866 Homo sapi
c	11	793.2	43.8	101458	2	AP000680	AP000680 Homo sapi
	12	717.4	39.6	736	9	AF277292	AF277292 Homo sapi
	13	531.2	29.3	637	6	AX136493	AX136493 Sequence
c	14	453	25.0	541	6	AX136640	AX136640 Sequence
	15	441	24.3	441	6	AX332845	AX332845 Sequence
c	16	339	18.7	221961	10	AC073435	AC073435 Mus muscu
c	17	323.8	17.9	340	6	AX331694	AX331694 Sequence
c	18	323.8	17.9	340	6	AX333904	AX333904 Sequence
	19	183.2	10.1	81318	2	AC016125	AC016125 Homo sapi
	20	183.2	10.1	101458	2	AP000680	AP000680 Homo sapi
	21	162	8.9	187960	9	AP000866	AP000866 Homo sapi
c	22	132.8	7.3	637	9	HSA326182	AJ326182 Homo sapi
c	23	132.8	7.3	674	9	HSA329044	AJ329044 Homo sapi
c	24	120	6.6	698	9	HSA331517	AJ331517 Homo sapi
	25	79.8	4.4	46240	2	AC105958	AC105958 Mus muscu
c	26	75	4.1	81318	2	AC016125	AC016125 Homo sapi
c	27	71	3.9	674	9	HSA331520	AJ331520 Homo sapi
	28	70.8	3.9	125020	9	AF429315	AF429315 Homo sapi
c	29	70	3.9	611	9	HSA323034	AJ323034 Homo sapi
c	30	59.6	3.3	165556	2	AC087190	AC087190 Homo sapi
	31	58.2	3.2	1147	9	BC007313	BC007313 Homo sapi
	32	58.2	3.2	1161	6	AX056679	AX056679 Sequence
	33	58.2	3.2	1221	9	AK000460	AK000460 Homo sapi
c	34	58	3.2	125020	9	AF429315	AF429315 Homo sapi
	35	54.2	3.0	95209	2	AP004323	AP004323 Oryza sat
c	36	54.2	3.0	153292	2	AP003635	AP003635 Oryza sat
	37	51.4	2.8	7218	6	I66494	I66494 Sequence 14
c	38	51	2.8	51	6	AX161199	AX161199 Sequence
c	39	51	2.8	51	6	AX161201	AX161201 Sequence
	40	50.4	2.8	57245	2	AC068263	AC068263 Homo sapi
	41	50	2.8	50	6	AX076928	AX076928 Sequence
	42	49.6	2.7	144973	2	AC096689	AC096689 Oryza sat

c	43	49.4	2.7	51	6	AX161200	AX161200 Sequence
c	44	49	2.7	1614	6	AX239602	AX239602 Sequence
c	45	49	2.7	12425	6	AX239607	AX239607 Sequence

ALIGNMENTS

```
RESULT   1
AX076924
LOCUS         AX076924                1813 bp     DNA      linear    PAT
22-FEB-2001
DEFINITION  Sequence 36 from Patent WO0105836.
ACCESSION   AX076924
VERSION     AX076924.1  GI:13121579
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1813)
  AUTHORS   Botstein,D., Goddard,A., Gurney,A.L., Hillan,K.J., Roy,M.A. and
            Wood,W.I.
  TITLE     Polypeptidic compositions and methods for the treatment of tumors
  JOURNAL   Patent: WO 0105836-A 36 25-JAN-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1813
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      368 a    559 c    484 g    402 t
ORIGIN
```

Query Match 100.0%; Score 1813; DB 6; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT 60

Qy      61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA 120

Qy     121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GGGCCATGATTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG 180

Qy     181 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GGCTGAGTGCCCTCGCGCCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC 240

Qy     241 ggttgcaggcggtggagggagggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGG 300

Qy     301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG 360

Qy     361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT 420

Qy     421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA 480

Qy     481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG 540

Qy     541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC 600

Qy     601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA 660

Qy     661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG 720

Qy     721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG 780

Qy     781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CTGGAGTCTATGTCTGCAAGGCCCACAATGAGGTGGGCACTGCCCAATGTAATGTGACGC 840

Qy     841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG 900

Qy     901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 TTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGG 960

Qy     961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA 1020

Qy    1021 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTCACCTCCGCACGAGCCC 1080

Qy    1081 tccggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctcca 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCA 1140

Qy    1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    1141 GCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATAT 1200

Qy    1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA 1260

Qy    1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTA 1320

Qy    1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG 1380

Qy    1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCCACCTCTCTTTACTGTGGGAAA 1440

Qy    1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA 1500

Qy    1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG 1560

Qy    1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA 1620

Qy    1621 tctgtaccccaccccctatctaacaccaccccttggctcccactccagctccctgtattgat 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 TCTGTACCCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT 1680

Qy    1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT 1740

Qy    1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 TAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG 1800

Qy    1801 tttgtatgaaaaa 1813
           |||||||||||||
Db    1801 TTTGTATGAAAAA 1813
```

```
RESULT   2
AF361746
LOCUS        AF361746                1838 bp     mRNA     linear    PRI
07-MAY-2001
DEFINITION  Homo sapiens endothelial cell-selective adhesion molecule (ESAM)
            mRNA, complete cds.
ACCESSION   AF361746
VERSION     AF361746.1  GI:13959017
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1838)
  AUTHORS   Hirata,K.-I., Ishida,T., Penta,K., Rezaee,M., Yang,E.,
            Wohlgemuth,J. and Quertermous,T.
  TITLE     Cloning of an Immunoglobulin Family Adhesion Molecule Selectively
            Expressed by Endothelial Cells
  JOURNAL   J. Biol. Chem. 276 (19), 16223-16231 (2001)
   PUBMED   11279107
REFERENCE   2  (bases 1 to 1838)
  AUTHORS   Quertermous,T., Ishida,T. and Hirata,K.-i.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2001) Cardiovascular Medicine, Stanford
            University, 300 Pasteur Drive, Falk CVRC, Stanford, CA
94305-5406,
            USA
FEATURES             Location/Qualifiers
     source          1. .1838
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     gene            1. .1838
                     /gene="ESAM"
     CDS             139. .1311
                     /gene="ESAM"
                     /note="immunoglobulin superfamily; contains V and C2
                     domains"
                     /codon_start=1
                     /product="endothelial cell-selective adhesion molecule"
                     /protein_id="AAK51065.1"
                     /db_xref="GI:13959018"

/translation="MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVE

GGEVVLPAWYTLHGEVSSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVY
SMPSRNLSLRLEGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRL
QGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSM
AGVYVCKAHNEVGTAQCNVTLEVSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGK
ALEEPANDIKEDAIAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTPT
PSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVPVMMPAQSQAGSLV"
BASE COUNT      385 a    563 c    483 g    407 t
ORIGIN
```

```
  Query Match             99.8%;  Score 1809.8;  DB 9;  Length 1838;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1811;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps
0;

Qy      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     14 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT 73

Qy     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     74 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA 133

Qy    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    134 GGGCCATGATTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG 193

Qy    181 ggctgagtgccctcgcgccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240

Db    194 GGCTGAGTGCCCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC 253

Qy    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300

Db    254 GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGG 313

Qy    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360

Db    314 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG 373

Qy    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420

Db    374 AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT 433

Qy    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480

Db    434 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA 493

Qy    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540

Db    494 AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG 553

Qy    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600

Db    554 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC 613

Qy    601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660

Db    614 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA 673

Qy    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720

Db    674 GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG 733

Qy    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780

Db    734 CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG 793

Qy    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840

Db    794 CTGGAGTCTATGTCTGCAAGGCCCACAATGAGGTGGGCACTGCCCAATGTAATGTGACGC 853

Qy    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900

Db    854 TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG 913

Qy    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960

Db    914 TTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGG 973

Qy    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020

Db    974 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGAACCCTGCCCTGGCCCA 1033

Qy   1021 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1080

Db   1034 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTCACCTCCGCACGAGCCC 1093

Qy   1081 tccggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctcca 1140

Db   1094 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCA 1153

Qy   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200

Db   1154 GCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATAT 1213

Qy   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260

Db   1214 CCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA 1273

Qy   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320

Db   1274 TGATGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTA 1333

Qy   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380

Db   1334 AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG 1393

Qy   1381 ggaaagagtcacactcctgacccttagtactctgccccccacctctctttactgtgggaaa 1440

Db   1394 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCCACCTCTCTTTACTGTGGGAAA 1453

Qy   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500

Db   1454 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA 1513

Qy   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560

Db   1514 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG 1573

Qy   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggccccttga 1620

Db   1574 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA 1633

Qy   1621 tctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattgat 1680

Db   1634 TCTGTACCCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT 1693

Qy   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740

Db   1694 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT 1753

Qy   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800

Db   1754 TAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG 1813

Qy   1801 tttgtatgaaaaa 1813

Db   1814 TTTGTATGAAAAA 1826

RESULT   3
```

```
AX136161
LOCUS       AX136161                1821 bp    DNA     linear   PAT
30-MAY-2001
DEFINITION  Sequence 83 from Patent EP1067182.
ACCESSION   AX136161
VERSION     AX136161.1  GI:14272569
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1821)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
            Hayashi,K.
  TITLE     Secretory protein or membrane protein
  JOURNAL   Patent: EP 1067182-A 83 10-JAN-2001;
            Helix Research Institute (JP)
FEATURES             Location/Qualifiers
     source          1. .1821
/organism="Homo sapiens"
/db_xref="taxon:9606"
     CDS             137. .1309
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC39723.1"
/db_xref="GI:14272570"
/translation="MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVE
GGEVVLPAWYTLHGEVSSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVY
SMPSRNLSLRLEGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRL
QGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSM
AGVYVCKAHNEVGTAQCNVTLEVSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGK
ALEEPANDIKEDAIAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTPT
PSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVPVMVPAQSQAGSLV"
BASE COUNT      366 a    561 c    489 g    405 t
ORIGIN
```

```
  Query Match             99.8%;  Score 1809;  DB 6;  Length 1821;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1809;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy       1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT 71

Qy      61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA 131

Qy     121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     132 GGGCCATGATTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG 191

Qy     181 ggctgagtgccctcgcgccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     192 GGCTGAGTGCCCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC 251

Qy     241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     252 GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGG 311

Qy     301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     312 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG 371

Qy     361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     372 AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT 431

Qy     421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     432 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA 491

Qy     481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     492 AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG 551

Qy     541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     552 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC 611

Qy     601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     612 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA 671

Qy     661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     672 GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG 731

Qy     721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     732 CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG 791

Qy     781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     792 CTGGAGTCTATGTCTGCAAGGCCCACAATGAGGTGGGCACTGCCCAATGTAATGTGACGC 851

Qy     841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     852 TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG 911

Qy     901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     912 TTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGG 971

Qy     961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     972 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA 1031

Qy    1021 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1032 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTCACCTCCGCACGAGCCC 1091

Qy    1081 tccggccaccccatggccctcccaggcctggtgcattgaccccccacgcccagtctctcca 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   1092 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCA 1151

Qy   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1152 GCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATAT 1211

Qy   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1212 CCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA 1271

Qy   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1272 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTA 1331

Qy   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1332 AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG 1391

Qy   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1392 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCCACCTCTCTTTACTGTGGGAAA 1451

Qy   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1452 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA 1511

Qy   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1512 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG 1571

Qy   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1572 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA 1631

Qy   1621 tctgtaccccaccccctatctaacaccacccttggctcccactccagctccctgtattgat 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1632 TCTGTACCCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT 1691

Qy   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1692 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT 1751

Qy   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1752 TAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG 1811

Qy   1801 tttgtatga 1809
          |||||||||
Db   1812 TTTGTATGA 1820


RESULT   4
AX191598
LOCUS        AX191598                1816 bp     DNA      linear    PAT
15-AUG-2001
DEFINITION  Sequence 120 from Patent WO0149728.
ACCESSION   AX191598
VERSION     AX191598.1  GI:15209789
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1816)
  AUTHORS   Kato,S. and Kimura,T.
  TITLE     Human proteins having hydrophobic domains and dnas encoding these
            proteins
  JOURNAL   Patent: WO 0149728-A 120 12-JUL-2001;
            Protegene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP)
FEATURES             Location/Qualifiers
     source          1. .1816
/organism="Homo sapiens"
/db_xref="taxon:9606"
     CDS             134. .1306
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC51184.1"
/db_xref="GI:15209790"
/translation="MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVE
GGEVVLPAWYTLHGEVSSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVY
SMPSRNLSLRLEGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRL
QGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSM
AGVYVCKAHNEVGTAQCNVTLEVSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHCRGK
ALEEPANDIKEDAIAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTPT
PSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVPVMVPAQSQAGSLV"
BASE COUNT      362 a    560 c    488 g    406 t
ORIGIN


  Query Match             99.5%;  Score 1804.8;  DB 6;  Length 1816;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1806;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps
0;

Qy      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT 68

Qy     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA 128

Qy    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 GGGCCATGATTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG 188

Qy    181 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 GGCTGAGTGCCCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC 248

Qy    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGG 308

Qy    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    309 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG 368

Qy    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT 428

Qy    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    429 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA 488

Qy    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    489 AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG 548

Qy    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    549 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC 608

Qy    601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    609 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA 668

Qy    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    669 GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG 728

Qy    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    729 CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG 788

Qy    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    789 CTGGAGTCTATGTCTGCAAGGCCCACAATGAGGTGGGCACTGCCCAATGTAATGTGACGC 848

Qy    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    849 TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG 908

Qy    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    909 TTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACTGCCGGGGCAAGGCCCTGG 968

Qy    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    969 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA 1028

Qy   1021 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1029 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTCACCTCCGCACGAGCCC 1088

Qy   1081 tccggccaccccatggccctcccaggcctggtgcattgaccccacgcccagtctctcca 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1089 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCA 1148

Qy   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1149 GCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATAT 1208

Qy   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1209 CCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA 1268

Qy   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTA 1328

Qy   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   1329 AAGGATTTGGGGTCTCTCCTTCCTATAGGGGTCACCTCTAGCACAGAGGCCTGAGTCATG 1388

Qy   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1389 GGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCCACCTCTCTTTACTGTGGGAAA 1448

Qy   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1449 ACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGA 1508

Qy   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1509 ATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAG 1568

Qy   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1569 CTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGA 1628

Qy   1621 tctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattgat 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1629 TCTGTACCCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGAT 1688

Qy   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1689 ATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTAT 1748

Qy   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1749 TAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATG 1808

Qy   1801 tttgtatg 1808
          ||||||||
Db   1809 TTTGTATG 1816
```

```
RESULT   5
AX073678
LOCUS        AX073678                1831 bp     DNA      linear    PAT
06-FEB-2001
DEFINITION  Sequence 12 from Patent WO0104264.
ACCESSION   AX073678
VERSION     AX073678.1  GI:12710099
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1831)
```

```
  AUTHORS   Jones,K.A., Volkmuth,W. and Walker,M.G.
  TITLE     Atherosclerosis-associated genes
  JOURNAL   Patent: WO 0104264-A 12 18-JAN-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1831
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT      370 a    561 c    494 g    406 t
ORIGIN


  Query Match             97.1%;  Score 1760.4;  DB 6;  Length 1831;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 1807;  Conservative    0;  Mismatches    6;  Indels   13;  Gaps
3;

Qy      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db      3 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCACCTC 62

Qy     61 cggcacctgcaggtccgt-gcgtcccgcggct-ggcgcccctgactccgtcccggccagg 118
          |||||||||||||||| |||||||||||| |||||||||||||||||||||||||||||
Db     63 GGGCACCTGCAGGTCCGTGGCGTCCCGCGGCTGGGCGCCCCTGACTCCGTCCCGGCCAGG 122

Qy    119 gagggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcct 178
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 GAGGGCCATGATTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCT 182

Qy    179 ggggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaa 238
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 GGGGCTGAGTGCCCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAA 242

Qy    239 ccggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgg 298
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 CCGGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGG 302

Qy    299 ggaggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaa 358
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 GGAGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAA 362

Qy    359 agaaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagt 418
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    363 AGAAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGT 422

Qy    419 atccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccagga 478
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    423 ATCCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGA 482

Qy    479 gaaagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctag 538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    483 GAAAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAG 542

Qy    539 gggccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctg 598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    543 GGGCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTG 602

Qy    599 ccgtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaag 658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    603 CCGTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAG 662

Qy    659 gagtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctt 718
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    663 GAGTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTT 722

Qy    719 tgcaccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccat 778
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    723 TGCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCAT 782

Qy    779 ggctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgac 838
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    783 GGCTGGAGTCTATGTCTGCAAGGCCCACAATGAGGTGGGCACTGCCCAATGTAATGTGAC 842

Qy    839 gctggaagtgagcaca----------gggcctggagctgcagtggttgctggagctgtt 887
          ||||||||||||||||          ||||||||||||||||||||||||||||||||
Db    843 GCTGGAAGTGAGCACAGGTCAGTGAGGGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTT 902

Qy    888 gtgggtaccctggttggactggggttgctggctgggctggtcctcttgtaccaccgccgg 947
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    903 GTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGG 962

Qy    948 ggcaaggccctggaggagccagccaatgatatcaaggaggatgccattgctccccggacc 1007
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    963 GGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACC 1022

Qy   1008 ctgccctggcccaagagctcagacacaatctccaagaatgggacccttcctctgtcacc 1067
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1023 CTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTCACC 1082

Qy   1068 tccgcacgagccctccggccaccccatggccctcccaggcctggtgcattgaccccacg 1127
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1083 TCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACG 1142

Qy   1128 cccagtctctccagccaggccctgccctcaccaagactgcccacgacagatggggcccac 1187
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1143 CCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCAC 1202

Qy   1188 cctcaaccaatatcccccatccctggtggggtttcttcctctggcttgagccgcatgggt 1247
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1203 CCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGT 1262

Qy   1248 gctgtgcctgtgatggtgcctgcccagagtcaagctggctctctggtatgatgaccccac 1307
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1263 GCTGTGCCTGTGATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCAC 1322

Qy   1308 cactcattggctaaaggatttggggtctctccttcctataagggtcacctctagcacaga 1367
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1323 CACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGA 1382

Qy   1368 ggcctgagtcatgggaaagagtcacactcctgacccttagtactctgcccccacctctct 1427
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1383 GGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCCACCTCTCT 1442

Qy   1428 ttactgtgggaaaaccatctcagtaagacctaagtgtccaggagacagaaggagaagagg 1487
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1443 TTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGG 1502
```

```
Qy    1488 aagtggatctggaattgggaggagcctccacccacccctgactcctccttatgaagccag 1547
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1503 AAGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAG 1562

Qy    1548 ctgctgaaattagctactcaccaagagtgaggggcagagacttccagtcactgagtctcc 1607
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1563 CTGCTGAAATTAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCC 1622

Qy    1608 caggcccccttgatctgtaccccaccctatctaacaccacccttggctcccactccagc 1667
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1623 CAGGCCCCCTTGATCTGTACCCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGC 1682

Qy    1668 tccctgtattgatataacctgtcaggctggcttggttaggttttactggggcagaggata 1727
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1683 TCCCTGTATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATA 1742

Qy    1728 gggaatctcttattaaaactaacatgaaatatgtgttgttttcatttgcaaatttaaata 1787
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1743 GGGAATCTCTTATTAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATA 1802

Qy    1788 aagatacataatgtttgtatgaaaaa 1813
           |||||||||||||||||||| | |
Db    1803 AAGATACATAATGTTTGTATGAGATA 1828
```

RESULT 6
BC016868
LOCUS BC016868 1734 bp mRNA linear PRI 09-NOV-2001
DEFINITION Homo sapiens, clone MGC:17599 IMAGE:3850665, mRNA, complete cds.
ACCESSION BC016868
VERSION BC016868.1 GI:16877212
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1734)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 20 Row: m Column: 10.
FEATURES Location/Qualifiers
source 1. .1734
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:17599 IMAGE:3850665"
/tissue_type="Colon, adenocarcinoma"
/clone_lib="NIH_MGC_65"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
CDS 8. .1180
/codon_start=1
/product="Unknown (protein for MGC:17599)"
/protein_id="AAH16868.1"
/db_xref="GI:16877213"
/translation="MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVE
GGEVVLPAWYTLHGEVSSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVY
SMPSRNLSLRLEGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRL
QGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSM
AGVYVCKAHNEVGTAQCNVTLEVSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGK
ALEEPANDIKEDAIAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTPT
PSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVPVMVPAQSQAGSLV"
BASE COUNT 396 a 507 c 444 g 387 t
ORIGIN

Query Match 93.3%; Score 1691.8; DB 9; Length 1734;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1693; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

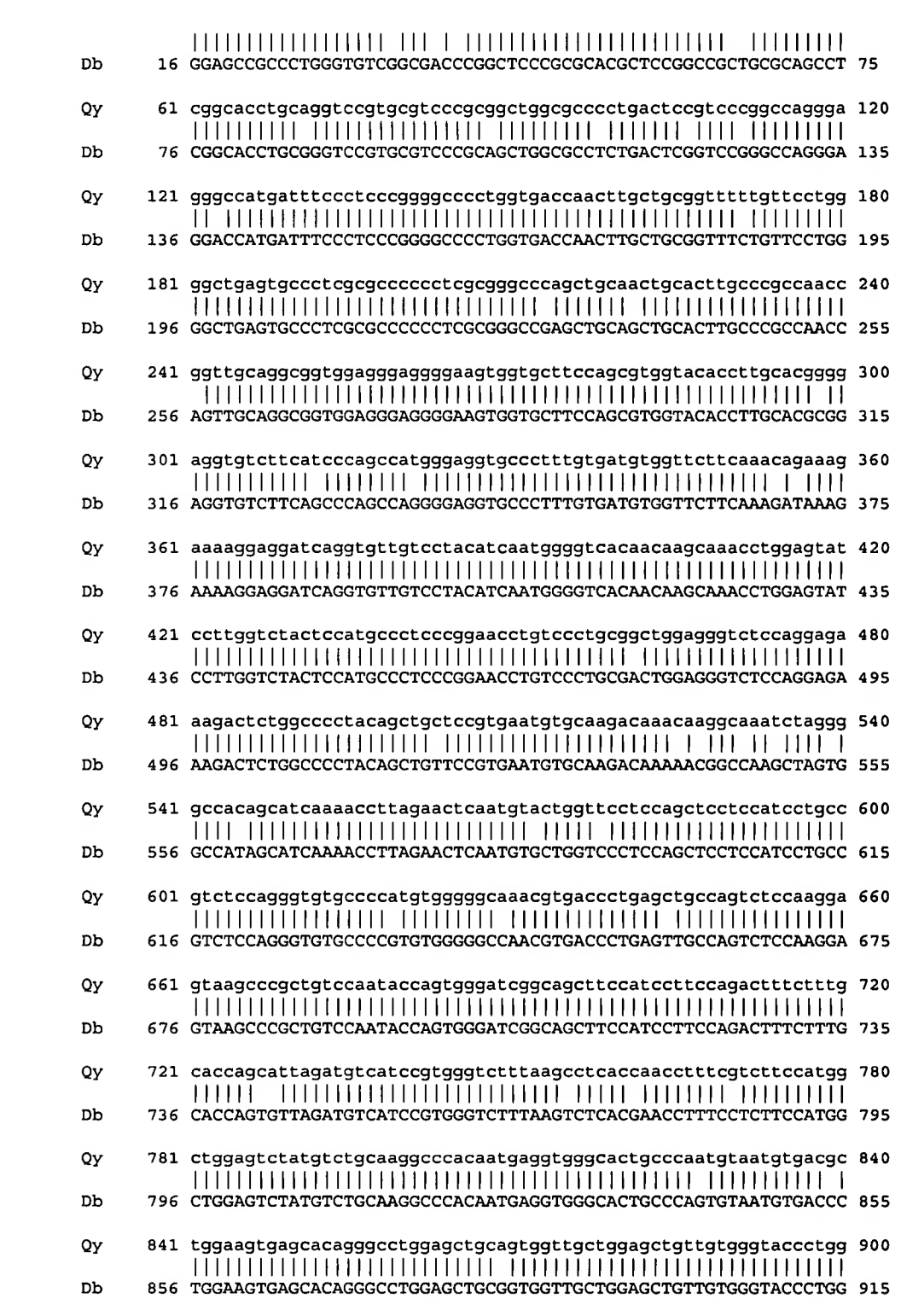
```
Qy     119 gagggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcct 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GAGGGCCATGATTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCT 60

Qy     179 ggggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaa 238
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGGGCTGAGTGCCCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAA 120

Qy     239 ccggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgg 298
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCGGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGG 180

Qy     299 ggaggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaa 358
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GGAGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAA 240

Qy     359 agaaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagt 418
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AGAAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGT 300

Qy     419 atccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccagga 478
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ATCCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGA 360
```

```
Qy    479 gaaagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctag 538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAAAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAG 420

Qy    539 gggccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctg 598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGGCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTG 480

Qy    599 ccgtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaag 658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCGTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAG 540

Qy    659 gagtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctt 718
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAGTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTT 600

Qy    719 tgcaccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccat 778
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TGCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCAT 660

Qy    779 ggctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgac 838
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GGCTGGAGTCTATGTCTGCAAGGCCCACAATGAGGTGGGCACTGCCCAATGTAATGTGAC 720

Qy    839 gctggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccct 898
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GCTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCT 780

Qy    899 ggttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccct 958
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGTTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCT 840

Qy    959 ggaggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggcc 1018
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCC 900

Qy   1019 caagagctcagacacaatctccaagaatgggacccttttcctctgtcacctccgcacgagc 1078
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CAAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTCACCTCCGCACGAGC 960

Qy   1079 cctccggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctc 1138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTC 1020

Qy   1139 cagccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaat 1198
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CAGCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAAT 1080

Qy   1199 atcccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgt 1258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGT 1140

Qy   1259 gatggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggc 1318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGC 1200

Qy   1319 taaaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtca 1378
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   1201 TAAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCA 1260

Qy   1379 tgggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtggga 1438
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCCACCTCTCTTTACTGTGGGA 1320

Qy   1439 aaaccatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctg 1498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTG 1380

Qy   1499 gaattgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaatt 1558
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATT 1440

Qy   1559 agctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccct 1618
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 AGCTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTT 1500

Qy   1619 gatctgtaccccaccccctatctaacaccaccccttggctcccactccagctccctgtattg 1678
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GATCTGTACCCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTG 1560

Qy   1679 atataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctctt 1738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTT 1620

Qy   1739 attaaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataa 1798
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 ATTAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAA 1680

Qy   1799 tgtttgtatgaaaaa 1813
          ||||||||||| | |
Db   1681 TGTTTGTATGAGATA 1695
```

```
RESULT   7
AB060855
LOCUS         AB060855                1855 bp     mRNA     linear    PRI
13-JUN-2001
DEFINITION  Macaca fascicularis brain cDNA clone:QtrA-11419, full insert
            sequence.
ACCESSION   AB060855
VERSION     AB060855.1  GI:13874503
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Macaca fascicularis adult male temporal lobe right cDNA to mRNA,
            clone_lib:macaque brain cDNA library QtrA clone:QtrA-11419.
  ORGANISM  Macaca fascicularis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (sites)
  AUTHORS   Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,
            Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
  TITLE     Isolation of full-length cDNA clones from macaque brain cDNA
            libraries
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1855)
  AUTHORS   Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
```

```
  TITLE     Direct Submission
  JOURNAL   Submitted (27-APR-2001) Katsuyuki Hashimoto, National Institute
of
            Infectious Diseases, Division of Genetic Resources; 23-1, Toyama
            1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
                                 (E-mail:khashi@nih.go.jp,
URL:http://www.nih.go.jp/yoken/genebank/,
            Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
COMMENT     Lab host:    TOP10
            Vector:      pME18S-FL3 (Acc.No. AB009864)
            R. Site1:    DraIII (CACTGTGTG)
            R. Site2:    DraIII (CACCATGTG)
           Description: 1st strand cDNA was primed with an oligo(dT) primer
           [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized
            using specific 5' and 3' primers and amplified by PCR. The PCR
            product was digested with SfiI and size selection was performed
to
           exclude fragments <1.5kb.The SfiI-digested PCR product was cloned
           into distinct DraIII sites of pME18S-FL3. XhoI sites just outside
               the DraIII sites can be used to isolate the cDNA insert.
Libraries
            were constructed by oligo-capping method
            (Sugano et al., , Institute of Medical Science, University of
            Tokyo).
            Custom primer used for sequencing
            ( 5' end primer [CTTCTGCTCTAAAAGCTGCG];
            3' end primer [CGACCTGCAGCTCGAGCACA] ).
FEATURES             Location/Qualifiers
     source          1. .1855
/organism="Macaca fascicularis"
/db_xref="taxon:9541"
/clone="QtrA-11419"
/sex="male"
/tissue_type="temporal lobe right"
/clone_lib="macaque brain cDNA library QtrA"
/dev_stage="adult"
     CDS             141. .1313
/codon_start=1
/product="hypothetical protein"
/protein_id="BAB46874.1"
/db_xref="GI:13874504"
/translation="MISLPGPLVTNLLRFLFLGLSALAPPSRAELQLHLPANQLQAVE
GGEVVLPAWYTLHAEVSSAQPGEVPFVMWFFKDKEKEDQVLSYINGVTTSKPGVSLVY
SMPSRNLSLRLEGLQEKDSGPYSCSVNVQDKNGQASGHSIKTLELNVLVPPAPPSCRL
QGVPRVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPVLDVIRGSLSLTNLSSSM
AGVYVCKAHNEVGTAQCNVTLEVSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGK
ALEEPANDIKEDAIAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTPT
PSLSSQALPSPRLPTTDGANPQPISLIPGGVSSSGLSRMGAVPVMVPAQSQAGSLV"
BASE COUNT      388 a    556 c    496 g    415 t
ORIGIN


  Query Match             91.5%;  Score 1659.6;  DB 9;  Length 1855;
  Best Local Similarity   95.4%;  Pred. No. 0;
  Matches 1731;  Conservative    0;  Mismatches   79;  Indels    4;  Gaps
2;

Qy      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
```



```
Qy    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    916 TTGGACTGGGGTTGCTGGCTGGGCTGGTCCTTTTGTACCACCGCCGGGGCAAGGCCCTGG 975

Qy    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    976 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA 1035

Qy   1021 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1036 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTCACCTCCGCACGAGCCC 1095

Qy   1081 tccggccacccccatggccctcccaggcctggtgcattgaccccccacgcccagtctctcca 1140
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1096 TCCGGCCACCCCCACGGCCCTCCCAGGCCTGGTGCATTGACCCCCCACGCCCAGTCTCTCCA 1155

Qy   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
          |||||||||||||||||||||||||||||| ||||| |||||| ||||||||||||||||
Db   1156 GCCAGGCCCTGCCCTCACCAAGACTGCCCACAACAGACGGGGCCAACCCTCAACCAATAT 1215

Qy   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
          | | |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1216 CTCTCATCCCTGGTGGAGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA 1275

Qy   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
          ||||||| |||||||||||||||||||||||| |||||||||| ||||||||||||||||
Db   1276 TGGTGCCCGCCCAGAGTCAAGCTGGCTCTCTGGTGTGATGACCCCGCCACTCATTGGCTA 1335

Qy   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
          |||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||
Db   1336 AAGGATTTGGGGTCTCTCTTTCCTATAGGGGTCACCTCTAGCACAGAGGCCTGAGTCATG 1395

Qy   1381 ggaaag-agtcacactcctgacccttagtactctgcccccacctctctttactgtgggaa 1439
          ||| || | ||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   1396 GGAGAGTAATCACACTCCAGACCCTTAGTACTCTGCCCCCACCTCTCTTTACTGTGGGAA 1455

Qy   1440 aaccatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgg 1499
          |||  |||||||||  |||||||||||||||||||  |||   ||||||||||||||||||||
Db   1456 AACTGTCTCAGTAACACCTAAGTGTCCAGGAGATAGA---AGAAGAGGAAGTGGATCTGG 1512

Qy   1500 aattgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaatta 1559
          |||||||||||||||||||||||||||||||||||| | ||||||||||||||||||||
Db   1513 AATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCCTGTGAAGCCAGCTGCTGAAATTA 1572

Qy   1560 gctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttg 1619
           || |||||||||||||| |||||||||||||||| |||||||||||||||||||| |||
Db   1573 ACTCCTCACCAAGAGTGAGTGGCAGAGACTTCCAGTTACTGAGTCTCCCAGGCCCCGTTG 1632

Qy   1620 atctgtaccccaccccctatctaacaccacccttggctcccactccagctccctgtattga 1679
          ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   1633 ATCTGTACCCCACCCCTATCTAACACCACCCTTTGCTCCCACTCCAGCTCCCTGTATTGA 1692

Qy   1680 tataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctctta 1739
          |||||||||||||||||||||||||||||||||||||||||||||||||||| | ||
Db   1693 TATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATGTATTT 1752

Qy   1740 ttaaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataat 1799
          || |||||||||||||||||||||||||||||||||||||||||| |||||||| |||||||
Db   1753 TTTAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTCAATAAAGACACATAAT 1812

Qy   1800 gtttgtatgaaaaa 1813
          || ||||||  | |
Db   1813 GTATGTATGGGATA 1826
```

RESULT 8
AX191588
LOCUS AX191588 1173 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 110 from Patent WO0149728.
ACCESSION AX191588
VERSION AX191588.1 GI:15209770
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Kato,S. and Kimura,T.
TITLE Human proteins having hydrophobic domains and dnas encoding these proteins
JOURNAL Patent: WO 0149728-A 110 12-JUL-2001;
Protegene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP)
FEATURES Location/Qualifiers
source 1. .1173
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 221 a 369 c 327 g 256 t
ORIGIN

Query Match 64.6%; Score 1171.4; DB 6; Length 1173;
Best Local Similarity 99.9%; Pred. No. 2.1e-261;
Matches 1172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy    126 atgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctggggctg 185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGATTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTG 60

Qy    186 agtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaaccggttg 245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGTGCCCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTG 120

Qy    246 caggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacggggaggtg 305
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTG 180

Qy    306 tcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaagaaaag 365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAG 240

Qy    366 gaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtatccttg 425
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTG 300
```

```
Qy    426 gtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggagaaagac 485
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGAC 360

Qy    486 tctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggggccac 545
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCAC 420

Qy    546 agcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgccgtctc 605
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTC 480

Qy    606 cagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaaggagtaag 665
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAG 540

Qy    666 cccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttgcacca 725
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCA 600

Qy    726 gcattagatgtcatccgtgggtctttaagcctcaccaaccttttcgtcttccatggctgga 785
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGA 660

Qy    786 gtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgctggaa 845
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GTCTATGTCTGCAAGGCCCACAATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAA 720

Qy    846 gtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctggttgga 905
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGA 780

Qy    906 ctggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctggaggag 965
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    781 CTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACTGCCGGGGCAAGGCCCTGGAGGAG 840

Qy    966 ccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggcccaagagc 1025
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGC 900

Qy   1026 tcagacacaatctccaagaatgggacccttttcctctgtcacctccgcacgagccctccgg 1085
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTCACCTCCGCACGAGCCCTCCGG 960

Qy   1086 ccaccccatggccctcccaggcctggtgcattgaccccccacgcccagtctctccagccag 1145
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCAGCCAG 1020

Qy   1146 gccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatatccccc 1205
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATATCCCCC 1080

Qy   1206 atccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtgatggtg 1265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGATGGTG 1140

Qy   1266 cctgcccagagtcaagctggctctctggtatga 1298
          |||||||||||||||||||||||||||||||
Db   1141 CCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGA 1173
```

```
RESULT   9
AF361882
LOCUS        AF361882                1840 bp    mRNA    linear   ROD
08-MAY-2001
DEFINITION  Mus musculus endothelial cell-selective adhesion molecule (Esam)
            mRNA, complete cds.
ACCESSION   AF361882
VERSION     AF361882.1  GI:13991772
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE   1  (bases 1 to 1840)
  AUTHORS   Hirata,K.-I., Ishida,T., Penta,K., Rezaee,M., Yang,E.,
            Wohlgemuth,J. and Quertermous,T.
  TITLE     Cloning of an immunoglobulin family adhesion molecule selectively
            expressed by endothelial cells
  JOURNAL   J. Biol. Chem. 276 (19), 16223-16231 (2001)
   PUBMED   11279107
REFERENCE   2  (bases 1 to 1840)
  AUTHORS   Quertermous,T., Ishida,T. and Hirata,K.-I.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAR-2001) Cardiovascular Medicine, Stanford
                 University, 300 Pasteur Drive, Falk CVRC, Stanford, CA
94305-5406,
            USA
FEATURES             Location/Qualifiers
     source          1. .1840
/organism="Mus musculus"
/strain="Swiss Webster/NIH"
/db_xref="taxon:10090"
/cell_type="endothelial"
     gene            1. .1840
/gene="Esam"
     CDS             118. .1302
/gene="Esam"
/note="ESAM; contains V and C2 domains; member of
immunoglobulin superfamily"
/codon_start=1
/product="endothelial cell-selective adhesion molecule"
/protein_id="AAK51504.1"
/db_xref="GI:13991773"
/translation="MILQAGTPETSLLRVLFLGLSTLAAFSRAQMELHVPPGLNKLEA
VEGEEVVLPAWYTMAREESWSHPREVPILIWFLEQEGKEPNQVLSYINGVMTNKPGTA
LVHSISSRNVSLRLGALQEGDSGTYRCSVNVQNDEGKSIGHSIKSIELKVLVPPAPPS
CSLQGVPYVGTNVTLNCKSPRSKPTAQYQWERLAPSSQVFFGPALDAVRGSLKLTNLS
IAMSGVYVCKAQNRVGFAKCNVTLDVMTGSKAAVVAGAVVGTFVGLVLIAGLVLLYQR
RSKTLEELANDIKEDAIAPRTLPWTKGSDTISKNGTLSSVTSARALRPPKAAPPRPGT
FTPTPSVSSQALSSPRLPRVDEPPPQAVSLTPGGVSSSALSRMGAVPVMVPAQSQAGS
LV"
BASE COUNT      404 a    498 c    482 g    456 t
ORIGIN
```

```
 Query Match             47.5%;  Score 861.6;  DB 10;  Length 1840;
 Best Local Similarity   73.3%;  Pred. No. 1.9e-189;
 Matches 1277;  Conservative    0;  Mismatches  424;  Indels   41;  Gaps
12;

Qy    108 tcccggccagggagggccatgatttccctcccggggcccctggtgaccaacttgctgcgg 167
          ||| ||||| |||||||||||||||    |   | ||  |||  | ||||| ||||||||||
Db    100 TCCGGGCCAAGGAGGGCCATGATTCTTCAGGCTGGAACCCCCGAGACCAGCTTGCTGCGG 159

Qy    168 tttttgttcctggggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcac 227
          |||||||||||||| |||||| |||| ||  ||  ||| || || ||| || |  |||||
Db    160 GTTTTGTTCCTGGGACTGAGTACCCTTGCTGCCTTCTCCCGAGCTCAGATGGAGTTGCAC 219

Qy    228 ttgcccgc------caaccggttgcaggcggtggagggaggggaagtggtgcttccagcg 281
           |||||  |      ||||   ||| | |||||| |||||||  |||||||||| || ||
Db    220 GTGCCCCCGGGCCTCAACAAATTGGAAGCGGTAGAGGGAGAAGAAGTGGTGCTCCCCGCC 279

Qy    282 tggtacaccttgcacggggaggtgtcttcatcccagccatgggaggtgccctttgtgatg 341
          ||||||||  ||    |||||| ||| |  ||||| ||  |||||||||| |  ||||
Db    280 TGGTACACGATGGCACGGGAGGAGTCGTGGTCCCACCCCCGGGAGGTGCCCATCCTGATC 339

Qy    342 tggttcttcaaacagaaagaaaagga---ggatcaggtgttgtcctacatcaatggggtc 398
          ||||||||  ||||  |||  |||||     | ||||||||||| ||||| ||||| |||
Db    340 TGGTTCTTGGAACAAGAAGGGAAGGAACCAAACCAGGTGTTGTCTTACATTAATGGAGTC 399

Qy    399 acaacaagcaaacctggagtatccttggtctactccatgccctcccggaacctgtccctg 458
          |  ||||  |||||||||  | || ||||| |||| ||  | || |||||  ||||||||
Db    400 ATGACAAATAAACCTGGAACAGCCCTGGTCCACTCTATCTCTTCACGGAATGTGTCCCTG 459

Qy    459 cggctggagggtctccaggagaaagactctggcccctacagctgctccgtgaatgtgcaa 518
          || |||| ||  |||||||||  |||||||||  | ||| |||| || || ||||||||
Db    460 CGCCTGGGGGCACTCCAGGAGGGAGACTCTGGGACTTACCGCTGTTCTGTCAATGTGCAG 519

Qy    519 gacaaacaaggcaaatctaggggccacagcatcaaaaccttagaactcaatgtactggtt 578
          |  |  |||||||| ||  |||||||||||||||| | |||| ||||| || ||||||
Db    520 AATGATGAAGGCAAAAGTATAGGCCACAGCATCAAAAGCATAGAGCTCAAAGTGCTGGTT 579

Qy    579 cctccagctcctccatcctgccgtctccagggtgtgccccatgtgggggcaaacgtgacc 638
          ||||||||||||||||||||  || | |||||||| ||| |||| ||| | || ||||||
Db    580 CCTCCAGCTCCTCCATCCTGTAGTTTACAGGGTGTACCCTATGTCGGGACCAATGTGACC 639

Qy    639 ctgagctgccagtctccaaggagtaagcccgctgtccaataccagtgggatcggcagctt 698
          |||| |||| |||| |||||||||| ||  |||  || ||||||||||  ||| |
Db    640 CTGAACTGCAAGTCCCCAAGGAGTAAACCTACTGCTCAGTACCAGTGGGAGAGGCTGGCC 699

Qy    699 ccatccttccagactttctttgcaccagcattagatgtcatccgtgggtctttaagcctc 758
          ||||||| ||||   ||||||| |||||| |||||||   | |||||  |||||||  |||
Db    700 CCATCCTCCCAGGTCTTCTTTGGACCAGCCTTAGATGCTGTTCGTGGATCTTTAAAGCTC 759

Qy    759 accaacctttcgtcttccatggctggagtctatgtctgcaaggcccacaatgaggtgggc 818
          || ||||||||   | ||||| ||||||||||||||||||||| || ||    ||||||
Db    760 ACTAACCTTTCCATTGCCATGTCTGGAGTCTATGTCTGCAAGGCTCAAAACAGAGTGGGC 819

Qy    819 actgcccaatgtaatgtgacgctggaagtgagcacagggcctggagctgcagtggttgct 878
           |||| | || || |||||  |||| ||||  ||||||  |    ||||||||||| |||
Db    820 TTTGCCAAGTGCAACGTGACCTTGGACGTGATGACAGGGTCCAAGGCTGCAGTGGTCGCT 879

Qy    879 ggagctgttgtgggtaccctggttggactggggttgctggctgggctggtcctcttgtac 938
          ||||| |||||||| ||  | |||||  ||| | || | |||||||||||||| ||||||
Db    880 GGAGCAGTTGTGGGCACTTTTGTTGGGTTGGTGCTGATAGCTGGGCTGGTCCTGTTGTAC 939

Qy    939 caccgccggggcaaggccctggaggagccagccaatgatatcaaggaggatgccattgct 998
          || |||||| ||||| || |||| ||||  |||||||||||||||||| ||||||||||
Db    940 CAGCGCCGGAGCAAGACCTTGGAAGAGCTGGCCAATGATATCAAGGAAGATGCCATTGCT 999

Qy    999 ccccggaccctgccctggcccaagagctcagacacaatctccaagaatgggacccttcc 1058
          |||||||| |||| ||| |||| |||||||||||||||||||||||||||||| |||||
Db   1000 CCCCGGACCTTGCCTTGGACCAAAGGCTCAGACACAATCTCCAAGAATGGGACACTTTCT 1059

Qy   1059 tctgtcacctccgcacgagccctccggccacccca---tggccctcccaggcctggtgca 1115
          || |||||||| |||||||| || ||||||||| |   ||  ||||| || |||||  ||
Db   1060 TCGGTCACCTCAGCACGAGCTCTGCGGCCACCCAAGGCTGCTCCTCCAAGACCTGGCACA 1119

Qy   1116 ttgacccccacgcccagtctctccagccaggccctgccctcaccaagactgcccacgaca 1175
          || || ||||| |||||| |||| |||||||||||| |||||||||||||||||| |  |
Db   1120 TTTACTCCCACACCCAGTGTCTCTAGCCAGGCCCTGTCCTCACCAAGACTGCCCAGGGTA 1179

Qy   1176 gatggggcccacccctcaaccaatatcccccatccctggtggggtttcttcctctggcttg 1235
          ||||  |||  ||||| || | ||||  | ||| |||||||||||||| ||||   ||
Db   1180 GATGAACCCCCACCTCAGGCAGTGTCCCTGACCCCAGGTGGGGTTTCTTCTTCTGCTCTG 1239

Qy   1236 agccgcatgggtgctgtgcctgtgatggtgcctgcccagagtcaagctggctctctggta 1295
          |||||||||||||||||||||||||||||||||||||| ||||||||  ||||| ||||| ||
Db   1240 AGCCGCATGGGTGCTGTGCCTGTGATGGTGCCTGCACAGAGTCAGGCTGGGTCTCTTGTG 1299

Qy   1296 tgatgaccccaccactcattggctaaaggatttggggtctctccttcctataagggtcac 1355
          ||||  |||   |||||||| ||||    || |||  |||  |||| || ||| |||| |
Db   1300 TGATAGCCCAGGCACTCATTAGCTA---CATCTGGTATCTGACCTTTCTGTAAAGGTCTC 1356

Qy   1356 c-tctagcacagaggcctgagtcatggga-aagagtcacactcctgacccttagtactct 1413
          | | | ||||||||| || | || |||||  |    |||| ||  ||||   ||| || |
Db   1357 CTTGTGGCACAGAGGACTCAATCTTGGGAGGATGCCCACATTCTAGACCTCCAGTCCTTT 1416

Qy   1414 gcccccacctctctttactgtgggaaaaccatctcagtaagacctaagtgtccaggagac 1473
          || || |||||  | || ||| |||| ||     |      |    |  ||  ||  |
Db   1417 GCTCCTACCTCCTTCTATTGTTGGAATACTGGGCCTCAGTAAGACTAAAATCTGGGTCAA 1476

Qy   1474 agaaggagaagaggaagtggatctggaattggg----------aggagcctccacccac 1522
          || |  | | |||||| |||| |||   | |||          |||||  || |||   |
Db   1477 AGGACAAAAGGAGGAAATGGACCTGAGGTAGGGGGTTGGGAGTAAGGAGGCTTCACTTCC 1536

Qy   1523 ccctgactcctcctt-----atgaagccagctgctgaaattagctactcaccaagagtga 1577
           ||   || |||| |       || |   |||||  |||  | |     |  | |  |
Db   1537 TCCCTGCTTCTCCCTGAAGCCAGATGAATGCTGCGGAAGATCGGCTACCCTCCAAGGGCT 1596

Qy   1578 ggggcagagacttccagtcactgagtctcccaggcccccttgatctgtaccccaccccta 1637
           ||  |||||| ||||||| |||    |||  | | |  |||||||||  ||||| ||
Db   1597 CTGGAGGAGACTGCCAGTCAGTGA--TGCCCCTGGCTCTGTGATCTGTACAACACCCTTA 1654

Qy   1638 tctaacaccacccttggctcc-cactccagctccctgtattgatataacctgtcaggctg 1696
          |||||  |   |||| ||    | ||||| |||||||||| ||||||||||  ||||
Db   1655 TCTAATGCTGTCCTTTGCCGTTCGCTCCATCTCCCTGTATTAATATAACCTGTCCTGCTG 1714

Qy   1697 gcttggttaggttttactggggca-gaggatagggaatctcttattaaaactaacatgaa 1755
          |||||| | |||||| ||  ||| | ||||||| ||    || | ||| || || ||||
Db   1715 GCTTGGCTGGGTTTTGTTGTAGCAGGGGGATAGGAAAGACATTTTAAAACCTGACTTGAA 1774
```

```
Qy   1756 atatgtgtt----gttttcatttgcaaatttaaataaagatacataatgtttgtatgaaa 1811
          ||   ||||     ||||  |||||||||||| ||||||||||||    |||| ||| ||
Db   1775 ATTGATGTTTTTGTTTTTATTTTGCAAATTTCAATAAAGATACATCGCATTTGCATGGAA 1834

Qy   1812 aa 1813
          ||
Db   1835 AA 1836
```

```
RESULT  10
AP000866/c
LOCUS       AP000866                187960 bp     DNA      linear    PRI
28-AUG-2001
DEFINITION  Homo sapiens genomic DNA, chromosome 11q, clone:RP11-677M14,
            complete sequence.
ACCESSION   AP000866
VERSION     AP000866.4  GI:15320462
KEYWORDS    HTG.
SOURCE      Homo sapiens DNA, clone:RP11-677M14.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 187960)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Homo sapiens genomic DNA
  JOURNAL   Published Only in Database (1999) In press
REFERENCE   2  (bases 1 to 187960)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
   JOURNAL    Submitted (13-DEC-1999) Masahira Hattori, The Institute of
Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
              1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045,
Japan
            (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     On Aug 27, 2001 this sequence version replaced gi:9845041.
FEATURES             Location/Qualifiers
     source          1. .187960
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
/clone="RP11-677M14"
BASE COUNT    53649 a  43111 c  40795 g  50405 t
ORIGIN
```

```
  Query Match             45.7%;  Score 828.2;  DB 9;  Length 187960;
  Best Local Similarity   99.6%;  Pred. No. 1.8e-181;
  Matches  830;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps
0;

Qy    981 aaggaggatgccattgctccccggaccctgccctggcccaagagctcagacacaatctcc 1040
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72580 AGGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCC 72521
```

```
Qy   1041 aagaatgggacccttcctctgtcacctccgcacgagccctccggccaccccatggccct 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72520 AAGAATGGGACCCTTTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCT 72461

Qy   1101 cccaggcctggtgcattgacccccacgcccagtctctccagccaggccctgccctcacca 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72460 CCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCA 72401

Qy   1161 agactgcccacgacagatggggcccaccctcaaccaatatcccccatccctggtggggtt 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72400 AGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATATCCCCCATCCCTGGTGGGGTT 72341

Qy   1221 tcttcctctggcttgagccgcatgggtgctgtgcctgtgatggtgcctgcccagagtcaa 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72340 TCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGATGGTGCCTGCCCAGAGTCAA 72281

Qy   1281 gctggctctctggtatgatgaccccaccactcattggctaaaggatttggggtctctcct 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72280 GCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCT 72221

Qy   1341 tcctataagggtcacctctagcacagaggcctgagtcatgggaaagagtcacactcctga 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72220 TCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGA 72161

Qy   1401 cccttagtactctgcccccacctctctttactgtgggaaaaccatctcagtaagacctaa 1460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72160 CCCTTAGTACTCTGCCCCCACCTCTCTTTACTGTGGGAAAACCATCTCAGTAAGACCTAA 72101

Qy   1461 gtgtccaggagacagaaggagaagaggaagtggatctggaattgggaggagcctccaccc 1520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72100 GTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATTGGGAGGAGCCTCCACCC 72041

Qy   1521 acccctgactcctccttatgaagccagctgctgaaattagctactcaccaagagtgaggg 1580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72040 ACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTACTCACCAAGAGTGAGGG 71981

Qy   1581 gcagagacttccagtcactgagtctcccaggcccccttgatctgtaccccaccccctatct 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  71980 GCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGATCTGTACCCCACCCCTATCT 71921

Qy   1641 aacaccacccttggctcccactccagctccctgtattgatataacctgtcaggctggctt 1700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  71920 AACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGGCTT 71861

Qy   1701 ggttaggttttactggggcagaggatagggaatctcttattaaaactaacatgaaatatg 1760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  71860 GGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTATTAAAACTAACATGAAATATG 71801

Qy   1761 tgttgttttcatttgcaaatttaaataaagatacataatgtttgtatgaaaaa 1813
          ||||||||||||||||||||||||||||||||||||||||||||||||||| | |
Db  71800 TGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATGTTTGTATGAGATA 71748
```

```
RESULT  11
AP000680/c
LOCUS       AP000680                101458 bp     DNA      linear    HTG
30-MAY-2000
DEFINITION  Homo sapiens chromosome 11 clone CMB9-25K9 map 11q24, WORKING
```

```
DRAFT
            SEQUENCE, 25 unordered pieces.
ACCESSION   AP000680
VERSION     AP000680.2  GI:8118868
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens DNA, clone:CMB9-25K9.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 101458)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama;A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Homo sapiens 101,458 genomic DNA of 11q24
  JOURNAL   Published Only in DataBase (1999) In press
REFERENCE   2  (bases 1 to 101458)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
   JOURNAL    Submitted (08-NOV-1999) Masahira Hattori, The Institute of
Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
            Japan (E-mail:hattori@gsc.riken.go.jp,
            URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
            Fax:81-42-778-9924)
COMMENT     On May 31, 2000 this sequence version replaced gi:6997554.
            -------------- Genome Center
                Center: RIKEN Genomic Sciences Center(GSC)
                Center code: RIKEN
                Web site: http://hgp.gsc.riken.go.jp/
                Contact: hattori@gsc.riken.go.jp
            -------------- Project Information
                Center project name: HumDraft11
                Center clone name: CMB9-25K9
            -------------- Summary Statistics
                Sequencing vector: PCR products; 100% of reads
                Chemistry: Dye-terminator ET-amersham; 100% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 89733 bases at least Q40
                Consensus quality: 95050 bases at least Q30
                Consensus quality: 97741 bases at least Q20
                Insert size: 99058; sum-of-contigs
                Quality coverage: 4.65x in Q20 bases; sum-of-contigs
            --------------.
            NOTE: This is a 'working draft' sequence. It currently consists
of
            25 contigs. The true order of the pieces is not known and their
            order in this sequence record is arbitrary. Gaps between the
             contigs are represented as runs N, but the exact sizes of the
gaps
               are unknown. This record will be updated with the finished
sequence
            as soon as it is available and the accession number will be
            preserved
1       9364 contig of   9364 bp in length
                 9465     16830 contig of   7366 bp in length
                16931     23631 contig of   6701 bp in length
                23732     29864 contig of   6133 bp in length
                29965     38284 contig of   8320 bp in length
                38385     44338 contig of   5954 bp in length
                44439     49484 contig of   5046 bp in length
                49585     55550 contig of   5966 bp in length
                55651     61139 contig of   5489 bp in length
                61240     65471 contig of   4232 bp in length
                65572     69042 contig of   3471 bp in length
                69143     73512 contig of   4370 bp in length
                73613     76146 contig of   2534 bp in length
                76247     79045 contig of   2799 bp in length
                79146     82078 contig of   2933 bp in length
                82179     83583 contig of   1405 bp in length
                83684     86476 contig of   2793 bp in length
                86577     89055 contig of   2479 bp in length
                89156     90922 contig of   1767 bp in length
                91023     92718 contig of   1696 bp in length
                92819     94573 contig of   1755 bp in length
                94674     95951 contig of   1278 bp in length
                96052     97799 contig of   1748 bp in length
                97900    100121 contig of   2222 bp in length
               100222    101458 contig of   1237 bp in length
Sequence updated (26-May-2000).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 25 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*        1     9364: contig of 9364 bp in length
*     9365 9464: gap of      100 bp
*     9465    16830: contig of 7366 bp in length
*    16831 16930: gap of      100 bp
*    16931    23631: contig of 6701 bp in length
*    23632 23731: gap of      100 bp
*    23732    29864: contig of 6133 bp in length
*    29865 29964: gap of      100 bp
*    29965    38284: contig of 8320 bp in length
*    38285 38384: gap of      100 bp
*    38385    44338: contig of 5954 bp in length
*    44339 44438: gap of      100 bp
*    44439    49484: contig of 5046 bp in length
*    49485 49584: gap of      100 bp
*    49585    55550: contig of 5966 bp in length
*    55551 55650: gap of      100 bp
*    55651    61139: contig of 5489 bp in length
*    61140 61239: gap of      100 bp
*    61240    65471: contig of 4232 bp in length
*    65472 65571: gap of      100 bp
*    65572    69042: contig of 3471 bp in length
*    69043 69142: gap of      100 bp
*    69143    73512: contig of 4370 bp in length
*    73513 73612: gap of      100 bp
*    73613    76146: contig of 2534 bp in length
*    76147 76246: gap of      100 bp
*    76247    79045: contig of 2799 bp in length
*    79046 79145: gap of      100 bp
```

```
            *    79146    82078: contig of 2933 bp in length
            *    82079 82178: gap of      100 bp
            *    82179    83583: contig of 1405 bp in length
            *    83584 83683: gap of      100 bp
            *    83684    86476: contig of 2793 bp in length
            *    86477 86576: gap of      100 bp
            *    86577    89055: contig of 2479 bp in length
            *    89056 89155: gap of      100 bp
            *    89156    90922: contig of 1767 bp in length
            *    90923 91022: gap of      100 bp
            *    91023    92718: contig of 1696 bp in length
            *    92719 92818: gap of      100 bp
            *    92819    94573: contig of 1755 bp in length
            *    94574 94673: gap of      100 bp
            *    94674    95951: contig of 1278 bp in length
            *    95952 96051: gap of      100 bp
            *    96052    97799: contig of 1748 bp in length
            *    97800 97899: gap of      100 bp
            *    97900   100121: contig of 2222 bp in length
            *   100122 100221: gap of      100 bp
            *   100222   101458: contig of 1237 bp in length.
FEATURES             Location/Qualifiers
     source          1. .101458
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q24"
/clone="CMB9-25K9"
     misc_feature    1. .9364
/note="assembly_fragment"
     misc_feature    9465. .16830
/note="assembly_fragment"
     misc_feature    16931. .23631
/note="assembly_fragment"
     misc_feature    23732. .29864
/note="assembly_fragment"
     misc_feature    29965. .38284
/note="assembly_fragment"
     misc_feature    38385. .44338
/note="assembly_fragment"
     misc_feature    44439. .49484
/note="assembly_fragment"
     misc_feature    49585. .55550
/note="assembly_fragment"
     misc_feature    55651. .61139
/note="assembly_fragment"
     misc_feature    61240. .65471
/note="assembly_fragment"
     misc_feature    65572. .69042
/note="assembly_fragment"
     misc_feature    69143. .73512
/note="assembly_fragment"
     misc_feature    73613. .76146
/note="assembly_fragment"
     misc_feature    76247. .79045
/note="assembly_fragment"
     misc_feature    79146. .82078
/note="assembly_fragment"
     misc_feature    82179. .83583
/note="assembly_fragment clone_end:T7 vector_side:right"
     misc_feature    83684. .86476
/note="assembly_fragment"
     misc_feature    86577. .89055
/note="assembly_fragment"
     misc_feature    89156. .90922
/note="assembly_fragment"
     misc_feature    91023. .92718
/note="assembly_fragment"
     misc_feature    92819. .94573
/note="assembly_fragment"
     misc_feature    94674. .95951
/note="assembly_fragment"
     misc_feature    96052. .97799
/note="assembly_fragment"
     misc_feature    97900. .100121
/note="assembly_fragment"
     misc_feature    100222. .101458
/note="assembly_fragment"
BASE COUNT    28116 a  21006 c  22205 g  27730 t   2401 others
ORIGIN


  Query Match             43.8%;  Score 793.2;  DB 2;  Length 101458;
  Best Local Similarity   99.3%;  Pred. No. 2.2e-173;
  Matches  828;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps
3;

Qy    981 aaggaggatgccattgctccccggaccctgccct-ggcccaagagctcagacacaatctc 1039
          | |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  57390 AGGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGGCCCAAGAGCTCAGACACAATCTC 57331

Qy   1040 caagaatgggacccttttcctctgtcacctccgcacgagccctccggccaccccatggccc 1099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  57330 CAAGAATGGGACCCTTTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCC 57271

Qy   1100 tcccaggcctggtgcattgaccccacgcccagtctctccagccaggccctgccctcacc 1159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  57270 TCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACC 57211

Qy   1160 aagactgcccacgacagatggggcccaccctcaaccaatatcccccatccctggtggggt 1219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  57210 AAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATATCCCCCATCCCTGGTGGGGT 57151

Qy   1220 ttcttcctctggcttgagccgcatgggtgctgtgcctgtgatggtgcctgcccagagtca 1279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  57150 TTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGATGGTGCCTGCCCAGAGTCA 57091

Qy   1280 agctggctctctggtatgatgaccccaccactcattggctaaaggatttggggtctctcc 1339
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db  57090 AGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTAAAGGATTT-GGGTCTCTCC 57032

Qy   1340 ttcctataagggtcacctctagcacagaggcctgagtcatgggaaagagtcacactcctg 1399
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db  57031 TTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCAT-GGAAAGAGTCACACTCCTG 56973

Qy   1400 acccttagtactctgcccccacctctctttactgtgggaaaaccatctcagtaagaccta 1459
```

```
Db  56972 ACCCTTAGTACTCTGCCCCCACCTCTCTTTACTGTGGGAAAACCATCTCAGTAAGACCTA 56913

Qy   1460 agtgtccaggagacagaaggagaagaggaagtggatctggaattgggaggagcctccacc 1519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  56912 AGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATTGGGAGGAGCCTCCACC 56853

Qy   1520 caccccctgactcctccttatgaagccagctgctgaaattagctactcaccaagagtgagg 1579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  56852 CACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTACTCACCAAGAGTGAGG 56793

Qy   1580 ggcagagacttccagtcactgagtctcccaggcccccttgatctgtaccccaccctatc 1639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  56792 GGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGATCTGTACCCCACCCCTATC 56733

Qy   1640 taacaccacccttggctcccactccagctccctgtattgatataacctgtcaggctggct 1699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  56732 TAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGGCT 56673

Qy   1700 tggttaggttttactggggcagaggatagggaatctcttattaaaactaacatgaaatat 1759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  56672 TGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTATTAAAACTAACATGAAATAT 56613

Qy   1760 gtgttgttttcatttgcaaatttaaataaagatacataatgtttgtatgaaaaa 1813
          |||||||||||||||||||||||||||||||||||||||||||||||| | |
Db  56612 GTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATGTTTGTATGAGATA 56559
```

```
RESULT  12
AF277292
LOCUS       AF277292                736 bp     mRNA     linear    PRI
03-AUG-2000
DEFINITION  Homo sapiens C4orf1 mRNA.
ACCESSION   AF277292
VERSION     AF277292.1  GI:9664852
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 736)
  AUTHORS   Sim,D.L.C., Yeo,W.M. and Chow,V.T.K.
  TITLE     The novel human HUEL gene (C4orf1) encodes a protein that shares
               homology with the DNA-binding domain of the XPA DNA repair
protein
              and displays nuclear translocation in a cell cycle-dependent
manner
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 736)
  AUTHORS   Chow,V.T.K., Sim,D.L.C. and Yeo,W.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUN-2000) Microbiology, National University of
            Singapore, 5, Science Drive 2, Singapore 117597, Singapore
FEATURES             Location/Qualifiers
     source          1. .736
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="bone marrow"
     CDS             <1. .282
/note="interacts with HUEL gene product encoded by
sequence deposited under GenBank Accession Number
AF006621; similar to XPA DNA repair protein's DNA-binding
domain; C4orf1"
/codon_start=1
/product="unknown"
/protein_id="AAF97236.1"
/db_xref="GI:9664853"
/translation="QEWDPFLCHLRTSPPATPWPSQAWCIDPHAQSLQPGPALTKTAH
DRWGPPSTNIPHPWWGFFLWLEPHGCCACDGACPESSWLSGMMTPPLIG"
BASE COUNT      176 a    234 c    165 g    161 t
ORIGIN
```

```
  Query Match             39.6%;  Score 717.4;  DB 9;  Length 736;
  Best Local Similarity   99.9%;  Pred. No. 5.3e-156;
  Matches  718;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps
0;

Qy   1040 caagaatgggacccttcctctgtcacctccgcacgagccctccggccaccccatggccc 1099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CAAGAATGGGACCCTTTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCC 60

Qy   1100 tcccaggcctggtgcattgacccccacgcccagtctctccagccaggccctgccctcacc 1159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACC 120

Qy   1160 aagactgcccacgacagatggggcccaccctcaaccaatatcccccatccctggtggggt 1219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATATCCCCCATCCCTGGTGGGGT 180

Qy   1220 ttcttcctctggcttgagccgcatgggtgctgtgcctgtgatggtgcctgcccagagtca 1279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGATGGTGCCTGCCCAGAGTCA 240

Qy   1280 agctggctctctggtatgatgaccccaccactcattggctaaaggatttggggtctctcc 1339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCC 300

Qy   1340 ttcctataagggtcacctctagcacagaggcctgagtcatgggaaagagtcacactcctg 1399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTG 360

Qy   1400 acccttagtactctgcccccacctctctttactgtgggaaaaccatctcagtaagaccta 1459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCCTTAGTACTCTGCCCCCACCTCTCTTTACTGTGGGAAAACCATCTCAGTAAGACCTA 420

Qy   1460 agtgtccaggagacagaaggagaagaggaagtggatctggaattgggaggagcctccacc 1519
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    421 AGTGTCCAGGAGACAGAAGGAGAAGAAGAAGTGGATCTGGAATTGGGAGGAGCCTCCACC 480

Qy   1520 caccccctgactcctccttatgaagccagctgctgaaattagctactcaccaagagtgagg 1579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTACTCACCAAGAGTGAGG 540

Qy   1580 ggcagagacttccagtcactgagtctcccaggcccccttgatctgtaccccaccctatc 1639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db     541 GGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGATCTGTACCCCACCCCTATC 600

Qy    1640 taacaccacccttggctcccactccagctccctgtattgatataacctgtcaggctggct 1699
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGGCT 660

Qy    1700 tggttaggttttactggggcagaggatagggaatctcttattaaaactaacatgaaata 1758
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTATTAAAACTAACATGAAATA 719


RESULT  13
AX136493
LOCUS         AX136493                637 bp     DNA      linear    PAT
30-MAY-2001
DEFINITION  Sequence 415 from Patent EP1067182.
ACCESSION   AX136493
VERSION     AX136493.1  GI:14272897
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 637)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
            Hayashi,K.
  TITLE     Secretory protein or membrane protein
  JOURNAL   Patent: EP 1067182-A 415 10-JAN-2001;
            Helix Research Institute (JP)
FEATURES             Location/Qualifiers
     source          1. .637
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT      116 a    202 c    185 g    129 t      5 others
ORIGIN


  Query Match             29.3%;  Score 531.2;  DB 6;  Length 637;
  Best Local Similarity   95.8%;  Pred. No. 8.9e-113;
  Matches  576;  Conservative    0;  Mismatches   21;  Indels    4;  Gaps
3;

Qy       1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCT 71

Qy      61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA 131

Qy     121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     132 GGGCCATGATTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG 191

Qy     181 ggctgagtgccctcgcgcccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     192 GGCTGAGTGCCCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC 251

Qy     241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     252 GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGG 311

Qy     301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     312 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG 371

Qy     361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     372 AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT 431

Qy     421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     432 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAAGGAG 491

Qy     481 aagactctggcccctacagctgctccg-tgaatgtgcaagacaaac-aaggcaaatctag 538
           ||       | ||||||||||||||| |||||||||||||||||| ||||||||||||
Db     492 AAAGACTCTGGCCCTACAGCTGCTCCGTTGAATGTGCAAGACAAACAAAGGCAAATCTAA 551

Qy     539 gggccaca--gcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcc 596
           ||||||||       |||||||| |||||||||||||||||||||| ||| |||||||
Db     552 GGGCCACAAGCATCAAAAACCTTANAACTCAATGTACTGGTTCCTCCANCTCNTCCATCC 611

Qy     597 t 597
           |
Db     612 T 612


RESULT  14
AX136640/c
LOCUS         AX136640                541 bp     DNA      linear    PAT
30-MAY-2001
DEFINITION  Sequence 562 from Patent EP1067182.
ACCESSION   AX136640
VERSION     AX136640.1  GI:14273044
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 541)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
            Hayashi,K.
  TITLE     Secretory protein or membrane protein
  JOURNAL   Patent: EP 1067182-A 562 10-JAN-2001;
            Helix Research Institute (JP)
FEATURES             Location/Qualifiers
     source          1. .541
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT      153 a    120 c    110 g    141 t     17 others
ORIGIN


  Query Match             25.0%;  Score 453;  DB 6;  Length 541;
  Best Local Similarity   91.8%;  Pred. No. 1.3e-94;
  Matches  490;  Conservative    0;  Mismatches   42;  Indels    2;  Gaps
```

```
2;

Qy   1277 tcaagctggctctctggtatgatgaccccaccactcattggctaaaggatttggggtctc 1336
          | ||   || | | ||| | ||   |||||||| | ||||| ||||||| ||||||| |
Db    534 TTAAAGNGGTTTTTTGGNANGAGACCCCCACCANTNATTGGTTAAAGGA-TTGGGGTTTT 476

Qy   1337 tccttcctataagggtcacctctagcacagaggcctgagtcatgggaaagagtcacactc 1396
          ||||| |||||||||||||| | ||||||||||||||||||||||||||||||||||| ||
Db    475 TCCTTTCTATAAGGGTCACTTTTAGCACAGAGGCCTGAGTCATGGGAAAGAGTCACATTC 416

Qy   1397 ctgacccttagtactctgcccccacctctctttactgtgggaaaaccatctcagtaagac 1456
          |||||||||||| | ||||||||| | | |||| |||||||||||||| ||||||||||
Db    415 NTGACCCTTAGTATTNTGCCCCCACTTTTTTTTTANTGTGGGAAAACCATNTCAGTAAGAC 356

Qy   1457 ctaagtgt-ccaggagacagaaggagaagaggaagtggatctggaattgggaggagcctc 1515
          ||||||| |||||||||||||||||||||||||||||| ||||||||||||||| ||
Db    355 NTAAGTGTCCCAGGAGACAGAAGGAGAAGAGGAAGTGGATNTGGAATTGGGAGGAGCTTC 296

Qy   1516 cacccacccctgactcctccttatgaagccagctgctgaaattagctactcaccaagagt 1575
          |||||||||||| || |||||||||||||||||||||||||||||| ||||||||||
Db    295 CACCCACCCCTGATTCTTCCTTATGAAGCCAGCTGCTGAAATTAGCTANTCACCAAGAGT 236

Qy   1576 gaggggcagagacttccagtcactgagtctcccaggcccccttgatctgtaccccacccc 1635
          |||||||||||||||||||||||||||| |||||||||||||||| ||||||||||||
Db    235 GAGGGGCAGAGACTTCCAGTCACTGAGTTTCCCAGGCCCCCTTGATNTGTACCCCACCCC 176

Qy   1636 tatctaacaccacccttggctcccactccagctccctgtattgatataacctgtcaggct 1695
          ||| |||||||||||||| |||||||||| |||||||||||||||||||||||||||||
Db    175 TATNTAACACCACCCTTGGNTCCCACTCCAGNTCCCTGTATTGATATAACCTGTCAGGCT 116

Qy   1696 ggcttggttaggttttactggggcagaggatagggaatctcttattaaaactaacatgaa 1755
          |||||||||||||||||||||||||||||||||||| | ||||||||||||||||||||
Db    115 GGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATNTTTTATTAAAACTAACATGAA 56

Qy   1756 atatgtgttgttttcatttgcaaatttaaataaagatacataatgtttgtatga 1809
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     55 ATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAATGTTTGTATGA 2


RESULT  15
AX332845
LOCUS        AX332845                441 bp     DNA      linear    PAT
09-JAN-2002
DEFINITION  Sequence 3354 from Patent WO0194629.
ACCESSION   AX332845
VERSION     AX332845.1  GI:18123479
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
   TITLE      Cancer gene determination and therapeutic screening using
signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 3354 13-DEC-2001;
```

```
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .441
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT      118 a    118 c     96 g    109 t
ORIGIN


  Query Match             24.3%;  Score 441;  DB 6;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-92;
  Matches  441;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy   1356 ctctagcacagaggcctgagtcatgggaaagagtcacactcctgacccttagtactctgc 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTCTAGCACAGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGC 60

Qy   1416 ccccacctctctttactgtgggaaaaccatctcagtaagacctaagtgtccaggagacag 1475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCCCACCTCTCTTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAG 120

Qy   1476 aaggagaagaggaagtggatctggaattgggaggagcctccacccaccccctgactcctcc 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGGAGAAGAGGAAGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCC 180

Qy   1536 ttatgaagccagctgctgaaattagctactcaccaagagtgaggggcagagacttccagt 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TTATGAAGCCAGCTGCTGAAATTAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGT 240

Qy   1596 cactgagtctcccaggcccccttgatctgtaccccacccctatctaacaccacccttggc 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CACTGAGTCTCCCAGGCCCCCTTGATCTGTACCCCACCCCTATCTAACACCACCCTTGGC 300

Qy   1656 tcccactccagctccctgtattgatataacctgtcaggctggcttggttaggttttactg 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTG 360

Qy   1716 gggcagaggatagggaatctcttattaaaactaacatgaaatatgtgttgttttcatttg 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGGCAGAGGATAGGGAATCTCTTATTAAAACTAACATGAAATATGTGTTGTTTTCATTTG 420

Qy   1776 caaatttaaataaagatacat 1796
          ||||||||||||||||||||
Db    421 CAAATTTAAATAAAGATACAT 441


Search completed: August 19, 2002, 16:13:11
Job time: 4324 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 15:04:12 ; Search time 220.41 Seconds
(without alignments)
14122.616 Million cell updates/sec

Title: US-09-902-759-38
Perfect score: 1813
Sequence: 1 ggagccgccctgggtgtcag.....cataatgtttgtatgaaaaa 1813

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
1: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1813	100.0	1813	20	AAX52221	Protein PRO246 cDN
	2	1813	100.0	1813	20	AAX28436	EGF-like homologue
	3	1813	100.0	1813	21	AAA30052	Human PRO246 nucle
	4	1813	100.0	1813	22	AAS21412	Human cDNA sequenc
	5	1813	100.0	1813	22	AAF60372	PRO246 coding sequ
	6	1813	100.0	1813	22	AAC87040	Nucleotide sequenc
	7	1813	100.0	1813	22	AAF72379	Human PRO246 cDNA.
	8	1813	100.0	1813	22	AAC97441	Human angiogenesis
	9	1809	99.8	1821	22	AAF93785	Human cDNA encodin
	10	1806.6	99.6	1827	22	AAH02949	Human shear stress
	11	1804.8	99.5	1816	22	AAD12605	Human protein havi
	12	1802	99.4	1954	21	AAA23441	cDNA encoding huma
	13	1783.8	98.4	1932	21	AAZ65278	Human secreted pro
	14	1760.4	97.1	1831	22	AAC85076	Atherosclerosis-as
	15	1757.6	96.9	1869	22	AAF44978	Human INTERCEPT 25
	16	1756	96.9	1869	22	AAF45014	Human secreted pro
	17	1756	96.9	1869	22	AAF45015	Human secreted pro
	18	1756	96.9	1869	22	AAF45016	Human secreted pro
	19	1756	96.9	1869	22	AAF45017	Human secreted pro
c	20	1440.8	79.5	1748	22	ABA09181	Human viral recept
c	21	1440.8	79.5	1748	22	AAI59707	Human polynucleoti
	22	1376	75.9	1387	20	AAX87000	Human viral recept
	23	1083.2	59.7	1290	20	AAZ00447	Human secreted pro
	24	1069.8	59.0	1110	22	AAF44979	Human INTERCEPT 25
	25	1068.2	58.9	1110	22	AAF45046	Human secreted pro
	26	1068.2	58.9	1110	22	AAF45047	Human secreted pro
	27	1068.2	58.9	1110	22	AAF45048	Human secreted pro
	28	1068.2	58.9	1110	22	AAF45049	Human secreted pro
	29	1010.4	55.7	1606	22	AAI57921	Human polynucleoti
	30	863.2	47.6	1846	22	AAF45020	Murine secreted pr
	31	861.6	47.5	1846	22	AAF44981	Murine INTERCEPT 2
	32	861.6	47.5	1846	22	AAF45018	Murine secreted pr
	33	861.6	47.5	1846	22	AAF45021	Murine secreted pr
	34	860	47.4	1846	22	AAF45019	Murine secreted pr
	35	730.2	40.3	1182	22	AAF45052	Murine secreted pr
	36	728.6	40.2	1182	22	AAF44982	Murine INTERCEPT 2
	37	728.6	40.2	1182	22	AAF45050	Murine secreted pr
	38	728.6	40.2	1182	22	AAF45053	Murine secreted pr
	39	727	40.1	1182	22	AAF45051	Murine secreted pr
	40	578.4	31.9	1288	22	AAD10122	Mouse 10.3 kDa pro
	41	531.2	29.3	637	22	AAF93981	Primer specific fo
c	42	453	25.0	541	22	AAF94128	Primer specific fo
	43	257.2	14.2	571	22	AAH97944	Murine 7-transmemb
	44	226.4	12.5	564	22	AAH97943	Murine 7-transmemb
	45	208	11.5	533	22	AAH97945	Murine 7-transmemb

ALIGNMENTS

RESULT 1
AAX52221
ID AAX52221 standard; DNA; 1813 BP.

XX

AC AAX52221;

XX

DT 25-JUN-1999 (first entry)

XX

DE Protein PRO246 cDNA clone DNA35639-1172.

XX

KW Secreted protein; transmembrane protein; human; enterocolitis;
KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW congenital microvillus atrophy; skin disease; cell growth;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
KW anti-thrombotic; wound healing; tissue repair; ss.

XX

OS Homo sapiens.

XX

PN WO9914328-A2.

XX

PD 25-MAR-1999.

XX

PF 16-SEP-1998; 98WO-US19330.

XX

PR 25-NOV-1997; 97US-0066840.
PR 17-SEP-1997; 97US-0059113.
PR 17-SEP-1997; 97US-0059115.
PR 17-SEP-1997; 97US-0059117.
PR 17-SEP-1997; 97US-0059119.
PR 17-SEP-1997; 97US-0059121.
PR 17-SEP-1997; 97US-0059122.
PR 17-SEP-1997; 97US-0059184.
PR 18-SEP-1997; 97US-0059263.
PR 18-SEP-1997; 97US-0059266.
PR 15-OCT-1997; 97US-0062125.
PR 17-OCT-1997; 97US-0062285.
PR 17-OCT-1997; 97US-0062287.
PR 21-OCT-1997; 97US-0063486.
PR 24-OCT-1997; 97US-0062814.
PR 24-OCT-1997; 97US-0062816.
PR 24-OCT-1997; 97US-0063045.
PR 24-OCT-1997; 97US-0063120.
PR 24-OCT-1997; 97US-0063121.
PR 24-OCT-1997; 97US-0063127.
PR 24-OCT-1997; 97US-0063128.
PR 27-OCT-1997; 97US-0063329.
PR 27-OCT-1997; 97US-0063327.
PR 28-OCT-1997; 97US-0063541.
PR 28-OCT-1997; 97US-0063542.
PR 28-OCT-1997; 97US-0063544.
PR 28-OCT-1997; 97US-0063549.
PR 28-OCT-1997; 97US-0063550.
PR 28-OCT-1997; 97US-0063564.
PR 29-OCT-1997; 97US-0063435.
PR 29-OCT-1997; 97US-0063704.
PR 29-OCT-1997; 97US-0063732.
PR 29-OCT-1997; 97US-0063738.
PR 29-OCT-1997; 97US-0063734.
PR 29-OCT-1997; 97US-0064215.
PR 29-OCT-1997; 97US-0063735.
PR 31-OCT-1997; 97US-0063870.
PR 31-OCT-1997; 97US-0064103.
PR 03-NOV-1997; 97US-0064248.
PR 07-NOV-1997; 97US-0064809.
PR 12-NOV-1997; 97US-0065186.
PR 17-NOV-1997; 97US-0065846.
PR 18-NOV-1997; 97US-0065693.
PR 21-NOV-1997; 97US-0066120.
PR 21-NOV-1997; 97US-0066364.
PR 24-NOV-1997; 97US-0066772.
PR 24-NOV-1997; 97US-0066466.
PR 24-NOV-1997; 97US-0066770.
PR 24-NOV-1997; 97US-0066511.
PR 24-NOV-1997; 97US-0066453.

XX

PA (GETH) GENENTECH INC.

XX

PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;

XX

DR WPI; 1999-229533/19.
DR P-PSDB; AAY13351.

XX

PT New isolated human genes and polypeptides used in, e.g. treatment of
PT gastrointestinal ulceration

XX

PS Claim 2; Fig 16; 320pp; English.

XX

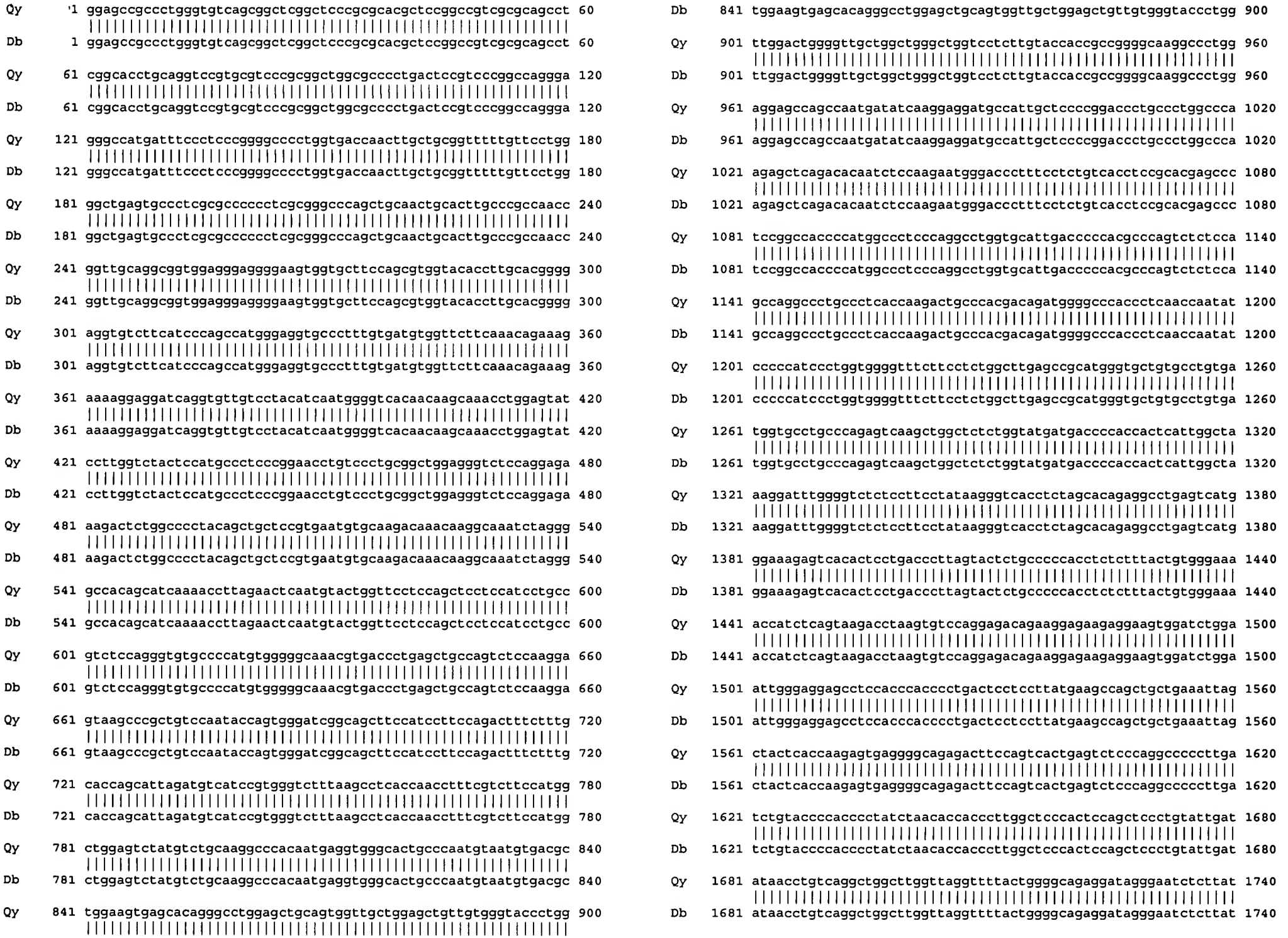
CC AAX52213-74 encode secreted and transmembrane human proteins, and are
CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
CC fetal brain, fetal liver and fetal retina. The encoded polypeptides
CC have specific uses based on their homology to known polypeptides,
CC e.g. PRO211 and PRO217 can be used for disorders associated with the
CC preservation and maintenance of gastrointestinal mucosa and the repair
CC of acute and chronic mucosal lesions (e.g. enterocolitis,
CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
CC microvillus atrophy), skin diseases associated with abnormal
CC keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as
CC lung squamous cell carcinoma of the vulva and gliomas), potent effects
on

CC cell growth and development, diseases related to growth or survival of
CC nerve cells including Parkinson's disease, Alzheimer's disease, ALS,
CC neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for
CC reducing dermal scarring. PRO264 can be used as a target for anti-tumor
CC drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia
CC areata; PRO269 can be used as an anti-thrombotic agent; PRO287
CC polypeptides and portions may have therapeutic applications in wound
CC healing and tissue repair; PRO317 can be used for treating problems of
CC the kidney, uterus, endometrium, blood vessels, or related tissue, e.g.
CC in the heart of genital tract.

XX

SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 20; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


Qy 1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
Db 1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
Qy 61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
Db 61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
Qy 121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
Db 121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
Qy 181 ggctgagtgccctcgcgcccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
Db 181 ggctgagtgccctcgcgcccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
Qy 241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
Db 241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
Qy 301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
Db 301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
Qy 361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
Db 361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
Qy 421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
Db 421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
Qy 481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
Db 481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
Qy 541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
Db 541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
Qy 601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
Db 601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
Qy 661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
Db 661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
Qy 721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
Db 721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
Qy 781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
Db 781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
Qy 841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
Db 841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
Qy 901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
Db 901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
Qy 961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
Db 961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
Qy 1021 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1080
Db 1021 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1080
Qy 1081 tccggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctcca 1140
Db 1081 tccggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctcca 1140
Qy 1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
Db 1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
Qy 1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
Db 1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
Qy 1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
Db 1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
Qy 1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
Db 1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
Qy 1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440
Db 1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440
Qy 1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500
Db 1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500
Qy 1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560
Db 1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560
Qy 1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620
Db 1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620
Qy 1621 tctgtaccccacccctatctaacaccaccccttggctcccactccagctccctgtattgat 1680
Db 1621 tctgtaccccacccctatctaacaccaccccttggctcccactccagctccctgtattgat 1680
Qy 1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740
Db 1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740

```
Qy   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800

Qy   1801 tttgtatgaaaaa 1813
          |||||||||||||
Db   1801 tttgtatgaaaaa 1813
```

RESULT 2
AAX28436
ID AAX28436 standard; DNA; 1813 BP.
XX
AC AAX28436;
XX
DT 22-JUN-1999 (first entry)
XX
DE EGF-like homologue PRO246 coding sequence.
XX
KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;
KW EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue;
KW FGF-8 homologue; ss.
XX
OS Homo sapiens.
XX
PN WO9914327-A2.
XX
PD 25-MAR-1999.
XX
PF 10-SEP-1998; 98WO-US18824.
XX
PR 25-NOV-1997; 97US-0066840.
PR 17-SEP-1997; 97US-0059114.
PR 17-SEP-1997; 97US-0059117.
PR 18-SEP-1997; 97US-0059263.
PR 15-OCT-1997; 97US-0062125.
PR 17-OCT-1997; 97US-0062285.
PR 17-OCT-1997; 97US-0062287.
PR 24-OCT-1997; 97US-0062816.
PR 29-OCT-1997; 97US-0063704.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney A, Hillan K, Lawrence DA;
PI Roy M, Wood WI;
XX
DR WPI; 1999-229532/19.
DR P-PSDB; AAY05286.
XX
PT Antibodies against specific proteins overexpressed in tumours
XX
PS Example 1; Fig 27; 130pp; English.
XX
CC This sequence encodes the EGF-like homologue PRO246.
CC The invention relates to antibodies (Ab) that bind to any of the
CC polypeptides (I) designated PRO187; PRO533; PRO214; PRO240; PRO211;
CC PRO230; PRO261; PRO246 or EBAF-2. The Ab, or other agents that inhibit
CC expression and/or activity of (I) are used: (i) to inhibit growth of
CC tumours; and (ii) as diagnostic/prognostic reagents for detection or
CC quantification of (I) in cells or tissues, by standard immunoassays, with
CC overexpression being indicative of cancer. For therapeutic use, the Ab
CC may be conjugated to a toxin, chemotherapeutic agent or radioisotope.
CC Genes expressing (I), many of which are growth factor homologues, are
CC overexpressed in some cases of cancer.
XX
SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 20; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60

Qy     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120

Qy    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180

Qy    181 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240

Qy    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300

Qy    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360

Qy    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420

Qy    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480

Qy    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540

Qy    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600

Qy    601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660

Qy    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720

Qy    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780

Qy    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840

Qy    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900

Qy    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960

Qy    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020

Qy   1021 agagctcagacacaatctccaagaatgggacccttttcctctgtcacctccgcacgagccc 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 agagctcagacacaatctccaagaatgggacccttttcctctgtcacctccgcacgagccc 1080

Qy   1081 tccggccaccccatggccctcccaggcctggtgcattgaccccacgcccagtctctcca 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 tccggccaccccatggccctcccaggcctggtgcattgaccccacgcccagtctctcca 1140

Qy   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200

Qy   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260

Qy   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320

Qy   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380

Qy   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440

Qy   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500

Qy   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560

Qy   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620

Qy   1621 tctgtaccccaccccctatctaacaccacccttggctcccactccagctccctgtattgat 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 tctgtaccccaccccctatctaacaccacccttggctcccactccagctccctgtattgat 1680

Qy   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740

Qy   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800

Qy   1801 tttgtatgaaaaa 1813
          |||||||||||||
Db   1801 tttgtatgaaaaa 1813
```

RESULT 3
AAA30052
ID AAA30052 standard; cDNA; 1813 BP.
XX
AC AAA30052;
XX
DT 09-AUG-2000 (first entry)
XX
DE Human PRO246 nucleotide sequence.
XX
KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;
KW PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human;
KW cell growth; proliferation; cell surface virus receptor; ADEPT;
KW antibody dependent enzyme mediated prodrug therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200015666-A2.
XX
PD 23-MAR-2000.
XX
PF 08-SEP-1999; 99WO-US20594.
XX
PR 10-SEP-1998; 98US-0099803.
PR 10-SEP-1998; 98WO-US18824.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI, Botstein D;
XX
DR WPI; 2000-271386/23.
DR P-PSDB; AAY88574.

XX

PT New isolated antibodies which bind to specific polypeptides used for
PT diagnosis and treatment of neoplastic cell growth and proliferation -
XX

PS Example 8; Fig 15; 200pp; English.
XX

CC This sequence represents a human PRO246 nucleotide sequence. PRO246 is
CC probably a cell surface virus receptor. The invention relates to
isolated
CC antibodies which bind to a polypeptide. The "PRO" polypeptides are
CC encoded by genes which are over expressed in the genome of tumour cells.
CC Vectors and host cells comprising the nucleic acid encoding the
CC antibodies are used in the production of the antibodies. The antibodies
CC and nucleic acids encoding them are used for diagnosing a tumour in a
CC mammal. The antibodies are used for inhibiting the growth of tumour
cells
CC and identifying compounds that inhibit a biological or immunological
CC activity of and/or expression of a PRO187, PRO533, PRO214, PRO240,
CC PRO211, PRO230, PRO261, PRO246 or PRO317 polypeptide. The antibody can
be
CC used in antibody dependent enzyme mediated prodrug therapy (ADEPT) by
CC conjugating the antibody to a prodrug-activating enzyme which converts
a
CC prodrug to an anti-cancer drug. The antibodies can be fluorescently
CC labelled and monitored by light microscopy, flow cytometry or
fluorimetry
CC for diagnosis and prognosis of tumours.
XX

SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 21; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps
0;

```
Qy      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60

Qy     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120

Qy    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180

Qy    181 ggctgagtgccctcgcgcccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ggctgagtgccctcgcgcccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240

Qy    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300

Qy    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360

Qy    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420

Qy    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480

Qy    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540

Qy    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600

Qy    601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660

Qy    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720

Qy    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780

Qy    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840

Qy    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900

Qy    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960

Qy    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020

Qy   1021 agagctcagacacaatctccaagaatgggacccttttcctctgtcacctccgcacgagccc 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 agagctcagacacaatctccaagaatgggacccttttcctctgtcacctccgcacgagccc 1080

Qy   1081 tccggccaccccatggccctcccaggcctggtgcattgaccccacgcccagtctctcca 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 tccggccaccccatggccctcccaggcctggtgcattgaccccacgcccagtctctcca 1140

Qy   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
```

```
Qy   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260

Qy   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320

Qy   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380

Qy   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440

Qy   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500

Qy   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560

Qy   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620

Qy   1621 tctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattgat 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 tctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattgat 1680

Qy   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740

Qy   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800

Qy   1801 tttgtatgaaaaa 1813
          |||||||||||||
Db   1801 tttgtatgaaaaa 1813
```

RESULT 4
AAS21412
ID AAS21412 standard; cDNA; 1813 BP.
XX
AC AAS21412;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human cDNA sequence encoding for PRO246 polypeptide.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal
muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32678.
XX
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR P-PSDB; AAU12340.
XX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical -
XX
PS Claim 3; Fig 337; 813pp; English.
XX
CC AAS21244-AAS21518 encode for novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing

CC PRO'polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 22; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
Db       1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60

Qy      61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
Db      61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120

Qy     121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
Db     121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180

Qy     181 ggctgagtgccctcgcgccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
Db     181 ggctgagtgccctcgcgccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240

Qy     241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
Db     241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300

Qy     301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
Db     301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360

Qy     361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
Db     361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420

Qy     421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
Db     421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480

Qy     481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
Db     481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540

Qy     541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
Db     541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600

Qy     601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
Db     601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660

Qy     661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
Db     661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720

Qy     721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
Db     721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780

Qy     781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
Db     781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840

Qy     841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
Db     841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900

Qy     901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
Db     901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960

Qy     961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
Db     961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020

Qy    1021 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1080
Db    1021 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1080

Qy    1081 tccggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctcca 1140
Db    1081 tccggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctcca 1140

Qy    1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
Db    1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200

Qy    1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
Db    1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260

Qy    1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
Db    1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320

Qy    1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
```

```
Db   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380

Qy   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440

Qy   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500

Qy   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560

Qy   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620

Qy   1621 tctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattgat 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 tctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattgat 1680

Qy   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740

Qy   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800

Qy   1801 tttgtatgaaaaa 1813
          |||||||||||||
Db   1801 tttgtatgaaaaa 1813
```

```
RESULT   5
AAF60372
ID   AAF60372 standard; cDNA; 1813 BP.
XX
AC   AAF60372;
XX
DT   27-APR-2001  (first entry)
XX
DE   PRO246 coding sequence.
XX
KW   Cytostatic; PRO protein; tumour; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200105836-A1.
XX
PD   25-JAN-2001.
XX
PF   20-DEC-1999;   99WO-US30999.
XX
PR   20-JUL-1999;   99US-0144758.
PR   26-JUL-1999;   99US-0145698.
PR   08-SEP-1999;   99WO-US20594.
PR   13-SEP-1999;   99WO-US20944.
PR   15-SEP-1999;   99WO-US21090.
PR   05-OCT-1999;   99WO-US23089.
PR   29-NOV-1999;   99WO-US28214.
PR   30-NOV-1999;   99WO-US28313.
PR   02-DEC-1999;   99WO-US28564.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Goddard A,  Gurney AL,  Hillan KJ,  Roy MA,  Wood WI;
XX
DR   WPI; 2001-091968/10.
DR   P-PSDB; AAB68599.
XX
PT   New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533,
PT   useful for diagnosing and treating cancers -
XX
PS   Claim 50; Fig 15; 196pp; English.
XX
CC   The present invention relates to PRO proteins and coding sequences. The
CC   present sequence is the coding sequence for one such PRO protein.
CC   It was found that the PRO genes are amplified in the genome of tumour
CC   cells. The gene amplification is expected to be associated with the
CC   overexpression of the gene product and contributes to tumourigenesis.
CC   Therefore, antagonists of PRO proteins are useful for the treatment of
CC   benign or malignant tumours, leukaemias, lymphoid malignancies and other
CC   disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
CC   epithelial, inflammatory and immunologic disorders.
XX
SQ   Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;
```

```
  Query Match             100.0%;  Score 1813;  DB 22;  Length 1813;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60

Qy     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120

Qy    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180

Qy    181 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240

Qy    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300

Qy    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
```

```
Db    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360

Qy    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420

Qy    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480

Qy    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540

Qy    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600

Qy    601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660

Qy    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720

Qy    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780

Qy    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840

Qy    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900

Qy    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960

Qy    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020

Qy   1021 agagctcagacacaatctccaagaatgggacccttttcctctgtcacctccgcacgagccc 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 agagctcagacacaatctccaagaatgggacccttttcctctgtcacctccgcacgagccc 1080

Qy   1081 tccggccaccccatggccctcccaggcctggtgcattgaccccacgcccagtctctccca 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 tccggccaccccatggccctcccaggcctggtgcattgaccccacgcccagtctctccca 1140

Qy   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200

Qy   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260

Qy   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320

Qy   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380

Qy   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440

Qy   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500

Qy   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560

Qy   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620

Qy   1621 tctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattgat 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 tctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattgat 1680

Qy   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740

Qy   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800

Qy   1801 tttgtatgaaaaa 1813
          |||||||||||||
Db   1801 tttgtatgaaaaa 1813
```

RESULT 6
AAC87040
ID AAC87040 standard; cDNA; 1813 BP.
XX
AC AAC87040;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of human polypeptide PRO246.
XX
KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361;
PRO1308;

KW PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
KW ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 126..1298
FT /*tag= a
FT sig_peptide 126..212
FT /*tag= b
XX
PN WO200077037-A2.
XX
PD 21-DEC-2000.
XX
PF 22-MAY-2000; 2000WO-US14042.
XX
PR 15-JUN-1999; 99US-0139695.
PR 20-JUL-1999; 99US-0145070.
PR 26-JUL-1999; 99US-0145698.
PR 17-AUG-1999; 99US-0149396.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28565.
PR 07-DEC-1999; 99US-0169495.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2001-050091/06.
DR P-PSDB; AAC87040.
XX
PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT transmembrane polypeptide is useful for gene therapy and identification
PT of related polypeptides -
XX
PS Claim 2; Fig 57; 244pp; English.
XX
CC The present sequence encodes a human secreted and transmembrane
CC polypeptide. The specification describes human polypeptides, designated
CC PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
CC PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC can be modulated with agents that bind to these polypeptides, resulting
CC in the death of the cells. The polynucleotides encoding these
CC polypeptides are useful in the recombinant production of the
CC polypeptides, as a hybridisation probe to screen libraries to isolate
CC homologous sequences, or to map the gene. They may also be used for
CC analysing genetic disorders, and to produce transgenic animals which are
CC useful for the development and screening of therapeutically useful
CC reagents. The polynucleotides can also be used in gene therapy e.g. to
CC replace a defective gene.
XX
SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 22; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60

Qy     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120

Qy    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180

Qy    181 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240

Qy    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300

Qy    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360

Qy    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420

Qy    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
```

```
Qy    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540

Qy    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600

Qy    601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660

Qy    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720

Qy    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780

Qy    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840

Qy    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900

Qy    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960

Qy    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020

Qy   1021 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1080

Qy   1081 tccggccaccccatggccctcccaggcctggtgcattgaccccacgcccagtctctcca 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 tccggccaccccatggccctcccaggcctggtgcattgaccccacgcccagtctctcca 1140

Qy   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200

Qy   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260

Qy   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320

Qy   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380

Qy   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440

Qy   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500

Qy   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560

Qy   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620

Qy   1621 tctgtaccccaccccctatctaacaccacccttggctcccactccagctccctgtattgat 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 tctgtaccccaccccctatctaacaccacccttggctcccactccagctccctgtattgat 1680

Qy   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740

Qy   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800

Qy   1801 tttgtatgaaaaa 1813
          |||||||||||||
Db   1801 tttgtatgaaaaa 1813
```

```
RESULT   7
AAF72379
ID   AAF72379 standard; cDNA; 1813 BP.
XX
AC   AAF72379;
XX
DT   24-APR-2001  (first entry)
XX
DE   Human PRO246 cDNA.
XX
KW   Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW   antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW   antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW   antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW   ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW   ischaemia; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200104311-A1.
XX
PD   18-JAN-2001.
XX
```

```
PF   22-FEB-2000; 2000WO-US04414.
XX
PR   07-JUL-1999;   99US-0143048.
PR   26-JUL-1999;   99US-0145698.
PR   28-JUL-1999;   99US-0146222.
PR   08-SEP-1999;   99WO-US20594.
PR   13-SEP-1999;   99WO-US20944.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   05-OCT-1999;   99WO-US23089.
PR   29-NOV-1999;   99WO-US28214.
PR   30-NOV-1999;   99WO-US28313.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30911.
PR   20-DEC-1999;   99WO-US30999.
PR   05-JAN-2000;   99WO-US00219.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N;
PI   Filvaroff E,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Grimaldi CJ,  Gurney AL,  Hillan KJ,  Kljavin IJ;
PI   Mather JP,  Pan J,  Paoni NF,  Roy MA,  Stewart TA,  Tumas D;
PI   Williams PM,  Wood WI;
XX
DR   WPI; 2001-081051/09.
DR   P-PSDB; AAB80219.
XX
PT   Sixty one nucleic acids encoding PRO polypeptides which are useful in
PT   the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
PT   squamous cell carcinoma) and neurodegenerative diseases (e.g.
PT   Alzheimer's disease) -
XX
PS   Claim 2; Fig 16; 393pp; English.
XX
CC   The present sequence is one of sixty one nucleic acids encoding novel
CC   secreted and transmembrane PRO polypeptides. The PRO polypeptides are
CC   useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
CC   squamous cell carcinoma), gastrointestinal disorders (e.g.
CC   enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
CC   Parkinson's disease), wound repair, cardiovascular disorders (e.g.
CC   endometrial bleeding angiogenesis, ischaemias such as coronary
CC   ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
CC   rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
CC   diabetes and retinal disorders such as retinitis pigmentosum.
CC   The PRO nucleic acids have applications in molecular biology, including
CC   use as hybridization probes, and in chromosome and gene mapping.
XX
SQ   Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;


  Query Match             100.0%;  Score 1813;  DB 22;  Length 1813;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1813;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps
0;

Qy      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60

Qy     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120

Qy    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180

Qy    181 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240

Qy    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300

Qy    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360

Qy    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420

Qy    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480

Qy    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540

Qy    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600

Qy°   601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660

Qy    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720

Qy    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780

Qy    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840

Qy    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
```

```
Qy    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960

Qy    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020

Qy   1021 agagctcagacacaatctccaagaatgggacccttttcctctgtcacctccgcacgagccc 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 agagctcagacacaatctccaagaatgggacccttttcctctgtcacctccgcacgagccc 1080

Qy   1081 tccggccaccccatggccctcccaggcctggtgcattgaccccacgcccagtctctccca 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 tccggccaccccatggccctcccaggcctggtgcattgaccccacgcccagtctctccca 1140

Qy   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200

Qy   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260

Qy   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320

Qy   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380

Qy   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440

Qy   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500

Qy   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560

Qy   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620

Qy   1621 tctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattgat 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 tctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattgat 1680

Qy   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740

Qy   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800

Qy   1801 tttgtatgaaaaa 1813
          |||||||||||||
Db   1801 tttgtatgaaaaa 1813
```

RESULT 8
AAC97441
ID AAC97441 standard; cDNA; 1813 BP.
XX
AC AAC97441;
XX
DT 28-FEB-2001 (first entry)
XX
DE Human angiogenesis-associated protein PRO246 cDNA, SEQ ID NO:95.
XX
KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
KW gene therapy; transgenic animal; ss.
XX
OS Homo sapiens.
XX
PN WO200053753-A2.
XX
PD 14-SEP-2000.
XX
PF 05-JAN-2000; 2000WO-US00219.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 14-MAY-1999; 99US-0134287.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2001-090793/10.
DR P-PSDB; AAB53082.

XX

PT New isolated nucleic acid for producing a PRO polypeptide, analyzing
PT genetic disorders and treating cardiovascular, endothelial or
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -

XX

PS Claim 58; Fig 37; 293pp; English.

XX

CC The invention relates to novel human angiogenesis-associated proteins
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
CC PRO proteins. The invention also relates to vectors and host cells
CC comprising a PRO nucleic acid, the recombinant production of a PRO
CC protein, PRO antibodies specific for a PRO protein, fusion proteins
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
CC compounds which inhibit the expression of a PRO gene. The invention
CC additionally encompasses methods of identifying modulators of PRO
CC expression or activity; diagnosing a cardiovascular, endothelial or
CC angiogenic disorder, or a susceptibility to such a disorder by detecting
CC mutations in a PRO gene, or the expression level of a PRO gene within a
CC particular tissue; treating a cardiovascular, endothelial or angiogenic
CC disorder via the administration of a PRO protein, PRO nucleic acid, or
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising
a
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
CC administration of a PRO protein, or an agonist or antagonist thereof.
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
CC agonists and PRO antagonists may be used as therapeutic agents to treat
CC cardiovascular, endothelial or angiogenic disorders, such as
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
CC disease, or stroke. PRO nucleic acids are additionally useful in the
CC recombinant production of PRO proteins, as hybridisation probes to
CC screen libraries to isolate cDNAs with sequence identity to PRO
proteins,
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in
CC gene therapy. PRO nucleic acids can also be used to produce transgenic
CC animals useful for the development and screening of potential
CC therapeutic agents. The present sequence represents a cDNA encoding a
PRO
CC protein of the invention.

XX

SQ Sequence 1813 BP; 368 A; 559 C; 484 G; 402 T; 0 other;

Query Match 100.0%; Score 1813; DB 22; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 0; Gaps
0;

```
Qy       1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60

Qy      61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120

Qy     121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180

Qy     181 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240

Qy     241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300

Qy     301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360

Qy     361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420

Qy     421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480

Qy     481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540

Qy     541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600

Qy     601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660

Qy     661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720

Qy     721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780

Qy     781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840

Qy     841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900

Qy     901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960

Qy     961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db     961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020

Qy    1021 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1080

Qy    1081 tccggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctcca 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 tccggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctcca 1140

Qy    1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200

Qy    1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260

Qy    1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320

Qy    1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380

Qy    1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440

Qy    1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500

Qy    1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560

Qy    1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620

Qy    1621 tctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattgat 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 tctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattgat 1680

Qy    1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740

Qy    1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800

Qy    1801 tttgtatgaaaaa 1813
           |||||||||||||
Db    1801 tttgtatgaaaaa 1813
```

```
RESULT   9
AAF93785
ID   AAF93785 standard; cDNA; 1821 BP.
XX
AC   AAF93785;
XX
DT   23-MAY-2001  (first entry)
XX
DE   Human cDNA encoding a membrane or secretory protein clone PSEC0086.
XX
KW   Human; secretory protein; membrane protein; vaccine; gene therapy;
KW   rheumatoid arthritis; diabetes; ss.
XX
OS   Homo sapiens.
XX
PN   EP1067182-A2.
XX
PD   10-JAN-2001.
XX
PF   07-JUL-2000; 2000EP-0114090.
XX
PR   08-JUL-1999;   99JP-0194179.
PR   11-JAN-2000; 2000JP-0118775.
PR   02-MAY-2000; 2000JP-0183766.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Kawai Y,  Sugiyama T,  Hayashi K;
XX
DR   WPI; 2001-093989/11.
DR   P-PSDB; AAB88358.
XX
PT   Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT   gene therapy or as candidate target molecules in drug development -
XX
PS   Claim 1; SEQ ID 83; 609pp + CD ROM; English.
XX
CC   This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC   which encode human secretory or membrane proteins represented by
CC   AAB88317 - AAB88419. Included in the invention are primers
CC    AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate
the
CC   cDNA sequences of the invention. The invention also includes methods for
CC   the production of antibodies directed against the proteins, and cDNA
CC   sequences, which can be used in vaccines. The polynucleotide sequences
CC   can be used in gene therapy. The polynucleotide sequences and the
CC   proteins they encode may be used in the prevention, treatment and
CC   diagnosis of diseases associated with inappropriate secretory
CC   protein/membrane protein expression. The nucleic acids and complementary
CC   sequences may also be used as DNA probes in diagnostic assays
CC   (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC   presence of similar nucleic acid sequences in samples. They may also be
CC   used to study the expression and function of secretory proteins/membrane
CC   polypeptides and their role in metabolism. The polypeptides may be used
CC   as antigens in the production of antibodies against them and in assays
to
CC   identify modulators (agonists and antagonists) of expression and
CC   activity. The antibodies and antagonists may also be used as therapeutic
```

CC agents to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA). Examples of diseases which may be treated include rheumatoid
CC arthritis and diabetes.
XX
SQ Sequence 1821 BP; 366 A; 561 C; 489 G; 405 T; 0 other;

Query Match 99.8%; Score 1809; DB 22; Length 1821;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     12 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 71

Qy     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     72 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 131

Qy    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    132 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 191

Qy    181 ggctgagtgccctcgcgcccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    192 ggctgagtgccctcgcgcccccctcgcgggcccagctgcaactgcacttgcccgccaacc 251

Qy    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    252 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 311

Qy    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    312 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 371

Qy    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    372 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 431

Qy    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    432 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 491

Qy    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    492 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 551

Qy    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    552 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 611

Qy    601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    612 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 671

Qy    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    672 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 731

Qy    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    732 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 791

Qy    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    792 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 851

Qy    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    852 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 911

Qy    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    912 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 971

Qy    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    972 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1031

Qy   1021 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1032 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1091

Qy   1081 tccggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctcca 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1092 tccggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctcca 1151

Qy   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1152 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1211

Qy   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1212 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1271

Qy   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1272 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1331

Qy   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1332 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1391

Qy   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1392 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1451

Qy   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1452 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1511

Qy   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   1512 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1571

Qy   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1572 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1631

Qy   1621 tctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattgat 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1632 tctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattgat 1691

Qy   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1692 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1751

Qy   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1752 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1811

Qy   1801 tttgtatga 1809
          |||||||||
Db   1812 tttgtatga 1820
```

RESULT 10
AAH02949
ID AAH02949 standard; DNA; 1827 BP.
XX
AC AAH02949;
XX
DT 15-JUN-2001 (first entry)
XX
DE Human shear stress-response coding sequence SEQ ID NO: 143.
XX
KW Human; shear stress-response protein; vascular disease;
KW arteriosclerosis; ds.
XX
OS Homo sapiens.
XX
PN WO200125427-A1.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-JP06840.
XX
PR 01-OCT-1999; 99JP-0280976.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (NOJI/) NOJIMA H.
XX
PI Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
PI Kuga T, Sekine S, Nakamura Y, Sugano S;
XX
DR WPI; 2001-266308/27.
DR P-PSDB; AAB90818.
XX
PT DNA sequences, proteins encoded by them and antibodies against them
PT useful in diagnosis and treatment of vascular disease caused by
PT arteriosclerosis -
XX
PS Claim 1; Page 595-599; 678pp; Japanese.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human shear stress response proteins. These are useful in the
CC diagnosis, treatment and screening of vascular diseases caused by
CC arteriosclerosis, including heart failure, post-PTCA restenosis and
CC hypertension.
XX
SQ Sequence 1827 BP; 369 A; 559 C; 491 G; 408 T; 0 other;

Query Match 99.6%; Score 1806.6; DB 22; Length 1827;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1809; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     13 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 72

Qy     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     73 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 132

Qy    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    133 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 192

Qy    181 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    193 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 252

Qy    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    253 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 312

Qy    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    313 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 372

Qy    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    373 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 432

Qy    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    433 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 492

Qy    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    493 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 552

Qy    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    553 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 612

Qy    601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
```

```
Db    613 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 672

Qy    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    673 gtaagcctgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 732

Qy    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    733 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 792

Qy    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    793 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 852

Qy    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    853 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 912

Qy    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    913 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 972

Qy    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    973 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1032

Qy   1021 agagctcagacacaatctccaagaatgggacccttttcctctgtcacctccgcacgagccc 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1033 agagctcagacacaatctccaagaatgggacccttttcctctgtcacctccgcacgagccc 1092

Qy   1081 tccggccaccccatggccctcccaggcctggtgcattgaccccacgcccagtctctcca 1140
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1093 tctggccaccccatggccctcccaggcctggtgcattgaccccacgcccagtctctcca 1152

Qy   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1153 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1212

Qy   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1213 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1272

Qy   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1273 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1332

Qy   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1333 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1392

Qy   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1393 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1452

Qy   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1453 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1512

Qy   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1513 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1572

Qy   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1573 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1632

Qy   1621 tctgtaccccaccccctatctaacaccacccttggctcccactccagctccctgtattgat 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1633 tctgtaccccaccccctatctaacaccacccttggctcccactccagctccctgtattgat 1692

Qy   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1693 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1752

Qy   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1753 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1812

Qy   1801 tttgtatgaaaaa 1813
          ||||||||| | |
Db   1813 tttgtatgagata 1825
```

RESULT 11
AAD12605
ID AAD12605 standard; cDNA; 1816 BP.
XX
AC AAD12605;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human protein having hydrophobic domain encoding cDNA clone HP10801.
XX
KW Human; hydrophobic domain; gene therapy; nutritional supplement;
KW cell proliferation; immunomodulatory; autoimmune disorder;
antimicrobial;
KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
KW haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
KW contraceptive; antiinfertility; antiinflammatory; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	134..1306
FT		/*tag= a
FT		/product= "Human protein having hydrophobic domain"
FT		/note= "CDS is specifically is claimed in claim 3"
FT	sig_peptide	134..223
FT		/*tag= b
FT	mat_peptide	224..1303
FT		/*tag= c
FT		/product= "Mature human protein with hydrophobic domain"

XX
PN WO200149728-A2.

XX

PD 12-JUL-2001.

XX

PF 28-DEC-2000; 2000WO-JP09359.

XX

PR 06-JAN-2000; 2000JP-0000585.
PR 06-JAN-2000; 2000JP-0000588.
PR 11-JAN-2000; 2000JP-0002299.
PR 03-FEB-2000; 2000JP-0026862.
PR 03-MAR-2000; 2000JP-0058367.

XX

PA (PROT-) PROTEGENE INC.
PA (SAGA) SAGAMI CHEM RES CENT.

XX

PI Kato S, Kimura T;

XX

DR WPI; 2001-418355/44.
DR P-PSDB; AAE06610.

XX

PT Human proteins with hydrophobic domains and the nucleic acids encoding
PT them, useful for preventing diagnosing and treating e.g. cancer,
PT Alzheimer's and inflammation -

XX

PS Claim 4; Page 486-489; 563pp; English.

XX

CC The present sequence is human protein with hydrophobic domain encoding
CC cDNA clone HP10801. The polynucleotide and polypeptide of the invention
CC may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The polynucleotides
CC may be used to produce the polypeptide, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the protein. The
CC polynucleotides and its complementary sequences may also be used as DNA
CC probes in diagnostic assays and also used in gene therapy. The
CC polypeptides may also be used as antigens in the production of antibodies
CC and in assays to identify modulators of polypeptide expression and
CC activity. The polypeptides and nucleic acids may be used as nutritional
CC supplements, to modulate cytokine and cell proliferation activity, to
CC modulate immune stimulation or suppression (e.g. for the treatment of
CC microbial infections and autoimmune disorders such as multiple sclerosis,
CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
CC haematopoiesis, to modulate tissue growth activity (e.g. for the
CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
CC disease), to modulate activin and inhibin activity (e.g. for controlling
CC fertility), to modulate chemotactic and chemokinetic activity, to
CC modulate haemostatic and thrombolytic activity, to modulate receptor
CC ligand activity, to modulate inflammation and to inhibit tumour growth.

XX

SQ Sequence 1816 BP; 362 A; 560 C; 488 G; 406 T; 0 other;

Query Match 99.5%; Score 1804.8; DB 22; Length 1816;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1806; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 68

Qy     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 128

Qy    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 188

Qy    181 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 248

Qy    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 308

Qy    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 368

Qy    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 428

Qy    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    429 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 488

Qy    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    489 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 548

Qy    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    549 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 608

Qy    601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    609 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 668

Qy    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    669 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 728

Qy    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    729 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 788

Qy    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    789 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 848

Qy    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    849 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 908

Qy    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    909 ttggactggggttgctggctgggctggtcctcttgtaccactgccggggcaaggccctgg 968

Qy    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    969 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1028

Qy   1021 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1029 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1088

Qy   1081 tccggccaccccatggccctcccaggcctggtgcattgaccccacgcccagtctctcca 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1089 tccggccaccccatggccctcccaggcctggtgcattgaccccacgcccagtctctcca 1148

Qy   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1149 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1208

Qy   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1209 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1268

Qy   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1328

Qy   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   1329 aaggatttggggtctctccttcctataggggtcacctctagcacagaggcctgagtcatg 1388

Qy   1381 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1389 ggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaa 1448

Qy   1441 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1449 accatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgga 1508

Qy   1501 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1509 attgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaattag 1568

Qy   1561 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1569 ctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttga 1628

Qy   1621 tctgtaccccaccccctatctaacaccacccttggctcccactccagctccctgtattgat 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1629 tctgtaccccaccccctatctaacaccacccttggctcccactccagctccctgtattgat 1688

Qy   1681 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1689 ataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttat 1748

Qy   1741 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1749 taaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatg 1808

Qy   1801 tttgtatg 1808
          ||||||||
Db   1809 tttgtatg 1816
```

RESULT 12
AAA23441
ID AAA23441 standard; cDNA; 1954 BP.
XX
AC AAA23441;
XX
DT 19-JUN-2000 (first entry)
XX
DE cDNA encoding human secreted protein vc51_1, SEQ ID NO:37.
XX
KW Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW neurodegenerative disease; asthma; contraceptive; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   139..1311
FT   /*tag= a
FT   /product= "Human secreted protein vc51_1"
XX
PN WO200011015-A1.
XX
PD 02-MAR-2000.
XX
PF 24-AUG-1999;   99WO-US19351.
XX
PR 24-AUG-1998;   98US-0097638.
PR 24-AUG-1998;   98US-0097659.
PR 09-SEP-1998;   98US-0099618.
PR 28-SEP-1998;   98US-0102092.
PR 25-NOV-1998;   98US-0109978.
PR 23-DEC-1998;   98US-0113645.
PR 23-DEC-1998;   98US-0113646.
PR 23-AUG-1999;   99US-0379246.
XX
PA (ALPH-) ALPHAGENE INC.
XX
PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-224657/19.
DR P-PSDB; AAY94999.
XX
PT New secreted or transmembrane proteins and polynucleotides encoding
PT them, useful for treating neurodegenerative disorders, autoimmune
PT diseases and cancer -
XX
PS Claim 46; Page 296; 357pp; English.

XX
CC The invention relates to 40 human secreted proteins (AAY94981-Y95020), CC and cDNA sequences encoding them (AAA23423-A23462). The secreted CC proteins of the invention include those that are thought to be only CC partially secreted, i.e., transmembrane proteins. The proteins of the CC invention may exhibit one or more activities selected from the following:
CC cytokine activity; cell proliferation; differentiation; immune CC modulation; haematopoiesis regulation; tissue growth activity; CC activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic CC and thrombolytic activity; anti-inflammatory activity; and tumour CC inhibition activity. The proteins may be administered to patients as CC vaccines, and the nucleotides may be used as part of a gene therapy CC regime. Diseases or conditions that may be treated using the proteins or CC nucleotides of the invention include autoimmune diseases; genetic CC disorders; haemophilia; cardiovascular diseases; cancer; bacterial, CC fungal and viral infections, especially HIV; multiple sclerosis; CC rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome; CC insulin dependent diabetes mellitus; and allergic reactions such as CC asthma and anaemia. They may also be used for treating wounds, burns, CC ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's CC disease, Parkinson's disease, Huntington's disease and amyotrophic CC lateral sclerosis (ALS). Proteins with activin/inhibin activity may CC additionally be useful as contraceptives. Nucleic acid sequences of the CC invention may be used in chromosome mapping, and as a source of CC diagnostic primers and probes. The present sequence represents cDNA CC encoding one of the 40 proteins of the invention.
XX
SQ Sequence 1954 BP; 498 A; 561 C; 490 G; 405 T; 0 other;

Query Match 99.4%; Score 1802; DB 21; Length 1954;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy       1 ggagccgccctgggtgtcagc-ggctcggctcccgcgcacgctccggccgtcgcgcagcc  59
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db      13 ggagccgccctgggtgtcagcgggctcggctcccgcgcacgctccggccgtcgcgcagcc  72

Qy      60 tcggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggg 119
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73 tcggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggg 132

Qy     120 agggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctg 179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     133 agggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctg 192

Qy     180 gggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaac 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     193 gggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaac 252

Qy     240 cggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacggg 299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     253 cggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacggg 312

Qy     300 gaggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaa 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     313 gaggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaa 372

Qy     360 gaaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagta 419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     373 gaaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagta 432

Qy     420 tccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggag 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     433 tccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggag 492

Qy     480 aaagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctagg 539
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     493 aaagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctagg 552

Qy     540 ggccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgc 599
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     553 ggccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgc 612

Qy     600 cgtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagg 659
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     613 cgtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagg 672

Qy     660 agtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttcttt 719
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     673 agtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttcttt 732

Qy     720 gcaccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatg 779
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     733 gcaccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatg 792

Qy     780 gctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacg 839
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     793 gctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacg 852

Qy     840 ctggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctg 899
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     853 ctggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctg 912

Qy     900 gttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctg 959
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     913 gttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctg 972

Qy     960 gaggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccc 1019
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     973 gaggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccc 1032

Qy    1020 aagagctcagacacaatctccaagaatgggacccttttcctctgtcacctccgcacgagcc 1079
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1033 aagagctcagacacaatctccaagaatgggacccttttcctctgtcacctccgcacgagcc 1092

Qy    1080 ctccggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctcc 1139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1093 ctccggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctcc 1152

Qy    1140 agccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaata 1199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1153 agccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaata 1212
```

```
Qy   1200 tcccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtg 1259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1213 tcccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtg 1272

Qy   1260 atggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggct 1319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1273 atggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggct 1332

Qy   1320 aaaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcat 1379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1333 aaaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcat 1392

Qy   1380 gggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaa 1439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1393 gggaaagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaa 1452

Qy   1440 aaccatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgg 1499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1453 aaccatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctgg 1512

Qy   1500 aattgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaatta 1559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1513 aattgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaatta 1572

Qy   1560 gctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttg 1619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1573 gctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttg 1632

Qy   1620 atctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattga 1679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1633 atctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattga 1692

Qy   1680 tataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctctta 1739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1693 tataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctctta 1752

Qy   1740 ttaaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataat 1799
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1753 ttaaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataat 1812

Qy   1800 gtttgtatgaaaaa 1813
           |||||||||||||
Db   1813 gtttgtatgaaaaa 1826
```

RESULT 13
AAZ65278
ID AAZ65278 standard; DNA; 1932 BP.
XX
AC AAZ65278;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human secreted protein gene 29.
XX
KW Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW therapy; ds.
XX
OS Homo sapiens.
XX
PN WO9958660-A1.
XX
PD 18-NOV-1999.
XX
PF 06-MAY-1999; 99WO-US09847.
XX
PR 12-MAY-1998; 98US-0085093.
PR 12-MAY-1998; 98US-0085094.
PR 12-MAY-1998; 98US-0085105.
PR 12-MAY-1998; 98US-0085180.
PR 18-MAY-1998; 98US-0085906.
PR 18-MAY-1998; 98US-0085920.
PR 18-MAY-1998; 98US-0085921.
PR 18-MAY-1998; 98US-0085922.
PR 18-MAY-1998; 98US-0085923.
PR 18-MAY-1998; 98US-0085924.
PR 18-MAY-1998; 98US-0085928.
PR 18-MAY-1998; 98US-0085925.
PR 18-MAY-1998; 98US-0085927.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR;
PI Lafleur DW, Endress GA, Ebner R;
XX
DR WPI; 2000-062296/05.
DR P-PSDB; AAY76152.
XX
PT New isolated human genes and the secreted polypeptides they encode,
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders -
XX
PS Claim 1; Page 313-314; 475pp; English.
XX
CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
CC AAY76124 to AAY76223 represent the secreted proteins encoded by the 97
CC human genes. The genes and their corresponding secreted polypeptides are
CC useful for preventing, treating or ameliorating medical conditions,
CC e.g. by protein or gene therapy. Also pathological conditions can be
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new genes. Specific
CC uses are described for each of the 97 genes, based on which tissues they
CC are most highly expressed in, and include developing products for the
CC diagnosis or treatment of cancer, tumours, developmental abnormalities
CC and foetal deficiencies, blood disorders, diseases of the immune system,
CC autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive
CC disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin
CC disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney
CC disorders, digestive/endocrine disorders, infections and AIDS. The
CC polypeptides are also useful for identifying their binding partners.

CC The sequences shown in AAY76224 to AAY76424 represent fragments of the
CC secreted proteins.
XX
SQ Sequence 1932 BP; 405 A; 585 C; 514 G; 424 T; 4 other;

Query Match 98.4%; Score 1783.8; DB 21; Length 1932;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1804; Conservative 3; Mismatches 1; Indels 2; Gaps 2;

```
Qy      4 gccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcctcgg 63
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| :|||||
Db      9 gccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgca-sctcgg 67

Qy     64 cacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccagggaggg 123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     68 cacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccagggaggg 127

Qy    124 ccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctggggc 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    128 ccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctggggc 187

Qy    184 tgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaaccggt 243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    188 tgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaaccggt 247

Qy    244 tgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacggggagg 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    248 tgcaggcggtggagggaggggaagtggtgcttccagcgtggtacanctgcacggggagg 307

Qy    304 tgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaagaaa 363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    308 tgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaagaaa 367

Qy    364 aggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtatcct 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368 aggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtatcct 427

Qy    424 tggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggagaaag 483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    428 tggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggagaaag 487

Qy    484 actctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggggcc 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    488 actctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggggcc 547

Qy    544 acagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgccgtc 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    548 acagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgccgtc 607

Qy    604 tccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaaggagta 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    608 tccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaaggagta 667

Qy    664 agcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttgcac 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    668 agcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttgcac 727

Qy    724 cagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatggctg 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    728 cagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatggctg 787

Qy    784 gagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgctgg 843
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    788 gagtctatgtctgcaaggcccacaatgaggtgggcactg-ccaatgtaatgtgacgctgg 846

Qy    844 aagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctggttg 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 aagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctggttg 906

Qy    904 gactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctggagg 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    907 gactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctggagg 966

Qy    964 agccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggcccaaga 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    967 agccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggcccaaga 1026

Qy   1024 gctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccctcc 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1027 gctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccctcc 1086

Qy   1084 ggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctccagcc 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1087 ggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctccagcc 1146

Qy   1144 aggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatatccc 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1147 aggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatatccc 1206

Qy   1204 ccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtgatgg 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1207 ccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtgatgg 1266

Qy   1264 tgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggctaaag 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1267 tgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggctaaag 1326

Qy   1324 gatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatggga 1383
          ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db   1327 gatttggggtctctccttcctatarggtcacctctagcacagaggcctgagtcatggga 1386

Qy   1384 aagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaaacc 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1387 aagagtcacactcctgacccttagtactctgcccccacctctctttactgtgggaaaacc 1446

Qy   1444 atctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctggaatt 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1447 atctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctggaatt 1506

Qy   1504 gggaggagcctccacccaccccctgactcctccttatgaagccagctgctgaaattagcta 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1507 gggaggagcctccacccaccccctgactcctccttatgaagccagctgctgaaattagcta 1566

Qy   1564 ctcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttgatct 1623
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   1567 ctcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccttgatct 1626

Qy   1624 gtaccccacccctatctaacaccacccttggctcccactccagctccctgtattgatata 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1627 gtaccccacccctatctaacaccacccttggctcccactccagctccctgtattgatata 1686

Qy   1684 acctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttattaa 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1687 acctgtcaggctggcttggttaggttttactggggcagaggatagggaatctcttattaa 1746

Qy   1744 aactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatgttt 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1747 aactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataatgttt 1806

Qy   1804 gtatgaaaaa 1813
          |||||||:|||
Db   1807 gtatgaraaa 1816
```

```
RESULT  14
AAC85076
ID   AAC85076 standard; DNA; 1831 BP.
XX
AC   AAC85076;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Atherosclerosis-associated gene seq ID No. 12.
XX
KW   Atherosclerosis-associated gene; stroke; myocardial infarction; human;
KW   ischemia; coronary artery disease; angina pectoris; hypertension;
KW   peripheral vascular disease; renal artery stenosis; antiatherosclerotic;
KW   cerebroprotective; cardiant; gene therapy; hypotensive; vasotropic;
KW   antianginal; ds.
XX
OS   Homo sapiens.
XX
PN   WO200104264-A2.
XX
PD   18-JAN-2001.
XX
PF   28-JUN-2000; 2000WO-US17887.
XX
PR   07-JUL-1999;   99US-0349015.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Jones KA,  Volkmuth W,  Walker MG;
XX
DR   WPI; 2001-138330/14.
XX
PT   Composition comprising atherosclerosis-associated polynucleotide useful
PT   in diagnosis, prognosis, treatment, and prevention of atherosclerosis
PT   and stroke, myocardial infarction, or hypertension  -
XX
PS   Claim 1; Page 43; 58pp; English.
XX
CC   The invention provides novel atherosclerosis-associated polynucleotides
CC   and polypeptides encoded by the genes. Expression vectors and host cells
CC   for producing the polypeptides are disclosed and methods for screening
or
CC   purifying ligands which specifically bind to the polypeptides are also
CC     provided. The polynucleotides are useful for treating diseases
associated
CC   with the altered expression of a gene that is coexpressed with one or
CC   more known atherosclerosis-associated genes in a subject. They are
CC   useful in diagnosis, prognosis, treatment, prevention, selection and
CC   evaluation of therapies for atherosclerosis including stroke, myocardial
CC   infarction, transient cerebral ischemia, mesenteric ischemia, coronary
CC   artery disease, angina pectoris, peripheral vascular disease, renal
CC   artery stenosis, and hypertension. Sequences AAC85065-85098 represent
CC   atherosclerosis-associated genes of the invention.
XX
SQ   Sequence 1831 BP; 370 A; 561 C; 494 G; 406 T; 0 other;
```

```
  Query Match             97.1%;  Score 1760.4;  DB 22;  Length 1831;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 1807;  Conservative    0;  Mismatches    6;  Indels   13;  Gaps
3;

Qy      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db      3 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcacctc 62

Qy     61 cggcacctgcaggtccgt-gcgtcccgcggct-ggcgcccctgactccgtcccggccagg 118
          |||||||||||||||| |||||||||||| |||||||||||||||||||||||||||||
Db     63 gggcacctgcaggtccgtggcgtcccgcggctgggcgcccctgactccgtcccggccagg 122

Qy    119 gagggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcct 178
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 gagggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcct 182

Qy    179 ggggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaa 238
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 ggggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaa 242

Qy    239 ccggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgg 298
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 ccggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgg 302

Qy    299 ggaggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaa 358
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 ggaggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaa 362

Qy    359 agaaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagt 418
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    363 agaaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagt 422

Qy    419 atccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccagga 478
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    423 atccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccagga 482

Qy    479 gaaagactctggccccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctag 538
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    483 gaaagactctggccccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctag 542
```

```
Qy    539 gggccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctg 598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    543 gggccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctg 602

Qy    599 ccgtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaag 658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    603 ccgtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaag 662

Qy    659 gagtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctt 718
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    663 gagtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctt 722

Qy    719 tgcaccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccat 778
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    723 tgcaccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccat 782

Qy    779 ggctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgac 838
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    783 ggctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgac 842

Qy    839 gctggaagtgagcaca----------gggcctggagctgcagtggttgctggagctgtt 887
          ||||||||||||||||          ||||||||||||||||||||||||||||||||
Db    843 gctggaagtgagcacaggtcagtgagggggcctggagctgcagtggttgctggagctgtt 902

Qy    888 gtgggtaccctggttggactggggttgctggctgggctggtcctcttgtaccaccgccgg 947
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    903 gtgggtaccctggttggactggggttgctggctgggctggtcctcttgtaccaccgccgg 962

Qy    948 ggcaaggccctggaggagccagccaatgatatcaaggaggatgccattgctccccggacc 1007
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    963 ggcaaggccctggaggagccagccaatgatatcaaggaggatgccattgctccccggacc 1022

Qy   1008 ctgccctggcccaagagctcagacacaatctccaagaatgggacccttcctctgtcacc 1067
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1023 ctgccctggcccaagagctcagacacaatctccaagaatgggacccttcctctgtcacc 1082

Qy   1068 tccgcacgagccctccggccaccccatggccctcccaggcctggtgcattgaccccacg 1127
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1083 tccgcacgagccctccggccaccccatggccctcccaggcctggtgcattgaccccacg 1142

Qy   1128 cccagtctctccagccaggccctgccctcaccaagactgcccacgacagatggggcccac 1187
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1143 cccagtctctccagccaggccctgccctcaccaagactgcccacgacagatggggcccac 1202

Qy   1188 cctcaaccaatatcccccatccctggtggggtttcttcctctggcttgagccgcatgggt 1247
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1203 cctcaaccaatatcccccatccctggtggggtttcttcctctggcttgagccgcatgggt 1262

Qy   1248 gctgtgcctgtgatggtgcctgcccagagtcaagctggctctctggtatgatgaccccac 1307
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1263 gctgtgcctgtgatggtgcctgcccagagtcaagctggctctctggtatgatgaccccac 1322

Qy   1308 cactcattggctaaaggatttggggtctctccttcctataagggtcacctctagcacaga 1367
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1323 cactcattggctaaaggatttggggtctctccttcctataagggtcacctctagcacaga 1382

Qy   1368 ggcctgagtcatgggaaagagtcacactcctgacccttagtactctgcccccacctctct 1427
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1383 ggcctgagtcatgggaaagagtcacactcctgacccttagtactctgcccccacctctct 1442

Qy   1428 ttactgtgggaaaaccatctcagtaagacctaagtgtccaggagacagaaggagaagagg 1487
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1443 ttactgtgggaaaaccatctcagtaagacctaagtgtccaggagacagaaggagaagagg 1502

Qy   1488 aagtggatctggaattgggaggagcctccacccacccctgactcctccttatgaagccag 1547
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1503 aagtggatctggaattgggaggagcctccacccacccctgactcctccttatgaagccag 1562

Qy   1548 ctgctgaaattagctactcaccaagagtgaggggcagagacttccagtcactgagtctcc 1607
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1563 ctgctgaaattagctactcaccaagagtgaggggcagagacttccagtcactgagtctcc 1622

Qy   1608 caggcccccttgatctgtaccccacccctatctaacaccacccttggctcccactccagc 1667
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1623 caggcccccttgatctgtaccccacccctatctaacaccacccttggctcccactccagc 1682

Qy   1668 tccctgtattgatataacctgtcaggctggcttggttaggttttactggggcagaggata 1727
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1683 tccctgtattgatataacctgtcaggctggcttggttaggttttactggggcagaggata 1742

Qy   1728 gggaatctcttattaaaactaacatgaaatatgtgttgttttcatttgcaaatttaaata 1787
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1743 gggaatctcttattaaaactaacatgaaatatgtgttgttttcatttgcaaatttaaata 1802

Qy   1788 aagatacataatgtttgtatgaaaaa 1813
          ||||||||||||||||||||| | |
Db   1803 aagatacataatgtttgtatgagata 1828
```

RESULT 15
AAF44978
ID AAF44978 standard; cDNA; 1869 BP.
XX
AC AAF44978;
XX
DT 28-MAR-2001 (first entry)
XX
DE Human INTERCEPT 258 coding sequence SEQ ID NO: 26.
XX
KW Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;
KW INTERCEPT 258; coronary disorder; olfactory disorder;
KW neurological disorder; pulmonary disorder; immunological disorder;
KW developmental disorder; kidney disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200078808-A1.
XX
PD 28-DEC-2000.
XX
PF 19-JUN-2000; 2000WO-US16883.
XX
PR 18-JUN-1999; 99US-0336536.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX

PI Leiby KR, McKay C, Bossone S;
XX
DR WPI; 2001-050109/06.
XX
PT New nucleic acids for treating diseases and disorders, e.g.
PT atherosclerosis, infection, autoimmune diseases, obesity, ear
PT disorders, brain disorders, tumors, diabetes, arthritis, multiple
PT sclerosis and asthma -
XX
PS Claim 1; Page 227; 332pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC human and murine secreted or transmembrane proteins TANGO 253, TANGO
257,
CC TANGO 281 and INTERCEPT 258. These are useful in the treatment of
CC coronary, pulmonary, olfactory, immunological, neurological,
CC developmental and kidney disorders.
XX
SQ Sequence 1869 BP; 391 A; 568 C; 496 G; 408 T; 6 other;

Query Match 96.9%; Score 1757.6; DB 22; Length 1869;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 22; Indels 2; Gaps
2;

```
Qy      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     28 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 87

Qy     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 147

Qy    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    148 gggccatgatttccctcccggggcccctggtgaccaacttgntgcggtttttgttcctgg 207

Qy    181 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    208 ggctgagtgccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaacc 267

Qy    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
          |||||||||||||||||  ||||||   |    | ||||  |||||||||||||| |||
Db    268 ggttgcaggcggtggaggaggggaaagtggtgcttcagcatggtacaccttgcacaggg 327

Qy    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    328 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 387

Qy    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 447

Qy    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    448 ccttggtctactccatgccctcccggaacctgtccctgcgggtggagggtctccaggaga 507

Qy    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 567

Qy    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 627

Qy    601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    628 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 687

Qy    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    688 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 747

Qy    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    748 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 807

Qy    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    808 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 867

Qy    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    868 tggaagtgagcacagggcctggagctgcagtggttgctgaagctgttgtgggtaccctgg 927

Qy    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    928 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 987

Qy    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    988 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1047

Qy   1021 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1048 agagctcagacacaatctccaagaatgggacccttcctctgtcacctccgcacgagccc 1107

Qy   1081 tccggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctcca 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   1108 tccggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctatcca 1167

Qy   1141 gccaggccctgccctcaccaagac-tgcccacgacagatggggcccaccctcaaccaata 1199
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   1168 gccaggccctgccctcaccaagacatgcccacgacagatggggcccaccctcaaccaata 1227

Qy   1200 tcccccatccctggtggggtttcttcctctggc-ttgagccgcatgggtgctgtgcctgt 1258
          |||||||||||||||||||| ||||| |||| ||||||||||||||||||| ||||||
Db   1228 tcccccatccctggtggggttttttccttggctttgagccgcatgggtgctgngcctgt 1287

Qy   1259 gatggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggc 1318
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1288 gatggngcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggc 1347

Qy   1319 taaaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtca 1378
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   1348 taaaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtca 1407

Qy   1379 tgggaaagagtcacactcctgacccttagtactctgccccccacctctctttactgtggga 1438
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1408 tgggaaagagtcacactcctgacccttagtactctgccccccacctctctttactgtggga 1467

Qy   1439 aaaccatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctg 1498
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1468 aaaccatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtggatctg 1527

Qy   1499 gaattgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaatt 1558
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1528 gaattgggaggagcctccacccacccctgactcctccttatgaagccagctgctgaaatt 1587

Qy   1559 agctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccctt 1618
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1588 agctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcccccctt 1647

Qy   1619 gatctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattg 1678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1648 gatctgtaccccacccctatctaacaccacccttggctcccactccagctccctgtattg 1707

Qy   1679 atataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctctt 1738
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1708 atataacctgtcaggctggcttggttaggttttactggggcagaggatagggaatctctt 1767

Qy   1739 attaaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataa 1798
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1768 attaaaactaacatgaaatatgtgttgttttcatttgcaaatttaaataaagatacataa 1827

Qy   1799 tgtttgtatgaaaaa 1813
           ||||||||||| | |
Db   1828 tgtttgtatgagata 1842
```

Search completed: August 19, 2002, 16:16:06
Job time: 4314 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 15:02:47 ; Search time 54.72 Seconds
(without alignments)
8138.405 Million cell updates/sec

Title: US-09-902-759-38
Perfect score: 1813
Sequence: 1 ggagccgccctgggtgtcag.....cataatgtttgtatgaaaaa 1813

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1376	75.9	1387	2	US-08-979-424-2	Sequence 2, Appli
	2	51.4	2.8	7218	1	US-08-232-463-14	Sequence 14, Appl
	3	45.4	2.5	1584	4	US-08-928-383B-1	Sequence 1, Appli
	4	45.4	2.5	2434	4	US-09-272-496-1	Sequence 1, Appli
	5	44.2	2.4	4403765	4	US-09-103-840A-2	Sequence 2, Appli
c	6	43.4	2.4	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	7	42.4	2.3	1095	4	US-08-928-383B-3	Sequence 3, Appli
c	8	42.2	2.3	2830	1	US-07-882-292-1	Sequence 1, Appli
c	9	42.2	2.3	2830	2	US-08-331-644-1	Sequence 1, Appli
c	10	42.2	2.3	2830	5	PCT-US93-04102-1	Sequence 1, Appli
c	11	41.8	2.3	477	4	US-09-135-994-1	Sequence 1, Appli
	12	41.6	2.3	1515	4	US-08-928-383B-25	Sequence 25, Appl
c	13	41.2	2.3	1280	4	US-09-060-756-4	Sequence 4, Appli
	14	41	2.3	4411529	4	US-09-103-840A-1	Sequence 1, Appli
	15	40.4	2.2	1355	3	US-08-415-655-14	Sequence 14, Appl
c	16	37.8	2.1	2576	1	US-08-471-033-35	Sequence 35, Appl
c	17	37.8	2.1	2576	2	US-08-471-044-35	Sequence 35, Appl
c	18	37.8	2.1	2576	2	US-08-463-483A-35	Sequence 35, Appl
c	19	37.8	2.1	2576	2	US-08-471-046A-35	Sequence 35, Appl
c	20	37.8	2.1	2576	2	US-08-470-566B-35	Sequence 35, Appl
c	21	37.8	2.1	2576	2	US-08-469-334-35	Sequence 35, Appl
c	22	37.8	2.1	2576	3	US-09-300-529-35	Sequence 35, Appl
c	23	37.8	2.1	2655	1	US-08-471-033-17	Sequence 17, Appl
c	24	37.8	2.1	2655	1	US-08-471-033-26	Sequence 26, Appl
c	25	37.8	2.1	2655	2	US-08-471-044-17	Sequence 17, Appl
c	26	37.8	2.1	2655	2	US-08-471-044-26	Sequence 26, Appl
c	27	37.8	2.1	2655	2	US-08-463-483A-17	Sequence 17, Appl
c	28	37.8	2.1	2655	2	US-08-463-483A-26	Sequence 26, Appl
c	29	37.8	2.1	2655	2	US-08-471-046A-17	Sequence 17, Appl
c	30	37.8	2.1	2655	2	US-08-471-046A-26	Sequence 26, Appl
c	31	37.8	2.1	2655	2	US-08-470-566B-17	Sequence 17, Appl
c	32	37.8	2.1	2655	2	US-08-470-566B-26	Sequence 26, Appl
c	33	37.8	2.1	2655	2	US-08-469-334-17	Sequence 17, Appl
c	34	37.8	2.1	2655	2	US-08-469-334-26	Sequence 26, Appl
c	35	37.8	2.1	2655	3	US-09-300-529-17	Sequence 17, Appl
c	36	37.8	2.1	2655	3	US-09-300-529-26	Sequence 26, Appl
c	37	37.8	2.1	4031	1	US-08-471-033-49	Sequence 49, Appl
c	38	37.8	2.1	4031	2	US-08-471-044-49	Sequence 49, Appl
c	39	37.8	2.1	4031	2	US-08-463-483A-49	Sequence 49, Appl
c	40	37.8	2.1	4031	2	US-08-471-046A-49	Sequence 49, Appl
c	41	37.8	2.1	4031	2	US-08-470-566B-49	Sequence 49, Appl
c	42	37.8	2.1	4031	2	US-08-469-334-49	Sequence 49, Appl
c	43	37.8	2.1	4031	3	US-09-300-529-49	Sequence 49, Appl
c	44	37.4	2.1	320	4	US-09-165-264-7	Sequence 7, Appli
c	45	37	2.0	1682	4	US-09-318-443-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-979-424-2
; Sequence 2, Application US/08979424
; Patent No. 5942606
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

```
;
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/979,424
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0405 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1387 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  LUNGFET03
;      CLONE:  1232054
US-08-979-424-2


  Query Match             75.9%;  Score 1376;  DB 2;  Length 1387;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1387;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps
1;

Qy      1 ggagccgccctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      1 GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCA-CCT 59

Qy     61 cggcacctgcaggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccaggga 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 CGGCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGA 119

Qy    121 gggccatgatttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctgg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 GGGCCATGATTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGG 179

Qy    181 ggctgagtgccctcgcgcccccctcgcgggcccagctgcaactgcacttgcccgccaacc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 GGCTGAGTGCCCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACC 239

Qy    241 ggttgcaggcggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacgggg 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 GGTTGCAGGCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGG 299

Qy    301 aggtgtcttcatcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaag 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 AGGTGTCTTCATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAG 359

Qy    361 aaaaggaggatcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtat 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 AAAAGGAGGATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTAT 419

Qy    421 ccttggtctactccatgccctcccggaacctgtccctgcggctggagggtctccaggaga 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 CCTTGGTCTACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGA 479

Qy    481 aagactctggcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggg 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 AAGACTCTGGCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGG 539

Qy    541 gccacagcatcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgcc 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 GCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCC 599

Qy    601 gtctccagggtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaagga 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 GTCTCCAGGGTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGA 659

Qy    661 gtaagcccgctgtccaataccagtgggatcggcagcttccatccttccagactttctttg 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 GTAAGCCCGCTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTG 719

Qy    721 caccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatgg 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 CACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGG 779

Qy    781 ctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgc 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 CTGGAGTCTATGTCTGCAAGGCCCACAATGAGGTGGGCACTGCCCAATGTAATGTGACGC 839

Qy    841 tggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctgg 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    840 TGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGG 899

Qy    901 ttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctgg 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    900 TTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGG 959

Qy    961 aggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    960 AGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCA 1019

Qy   1021 agagctcagacacaatctccaagaatgggacccttttcctctgtcacctccgcacgagccc 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1020 AGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTCACCTCCGCACGAGCCC 1079

Qy   1081 tccggccaccccatggccctcccaggcctggtgcattgacccccacgcccagtctctcca 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080 TCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCA 1139

Qy   1141 gccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaaccaatat 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 GCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATAT 1199

Qy   1201 cccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtga 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 CCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGA 1259
```

```
Qy   1261 tggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactcattggcta 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1260 TGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTA 1319

Qy   1321 aaggatttggggtctctccttcctataagggtcacctctagcacagaggcctgagtcatg 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1320 AAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATG 1379

Qy   1381 ggaaagag 1388
          ||||||||
Db   1380 GGAAAGAG 1387


RESULT   2
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14


  Query Match              2.8%;  Score 51.4;  DB 1;  Length 7218;
  Best Local Similarity    2.6%;  Pred. No. 0.00045;
  Matches   10;  Conservative  219;  Mismatches  150;  Indels    0;  Gaps
0;

Qy    981 aaggaggatgccattgctccccggaccctgccctggcccaagagctcagacacaatctcc 1040
          | ||||  ||| ||: ::::::   :::: :::: :::     :::   : :  :::::
Db   1053 AGGGAGCTTGCGATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1112

Qy   1041 aagaatgggacccttcctctgtcacctccgcacgagccctccggccaccccatggccct 1100
               :    :::::::::::: :: ::::: : :   ::::::  :: :::: :  ::::
Db   1113 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1172

Qy   1101 cccaggcctggtgcattgacccccacgcccagtctctccagccaggccctgccctcacca 1160
          :::   :::  : : ::  ::::: : :::  :::::::  ::   :::: ::::: ::
Db   1173 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1232

Qy   1161 agactgcccacgacagatggggcccaccctcaaccaatatcccccatccctggtggggtt 1220
             :: ::: :  :   :    ::: ::::::  ::  : :::::: ::::::  :    ::
Db   1233 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1292

Qy   1221 tcttcctctggcttgagccgcatgggtgctgtgcctgtgatggtgcctgcccagagtcaa 1280
          :::::::::  :::   :: : :   : :: : ::: :  :  : ::: :::    ::
Db   1293 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1352

Qy   1281 gctggctctctggtatgatgaccccaccactcattggctaaaggatttggggtctctcct 1340
           ::  ::::::  : :  :  :::: :: ::: ::  ::      :::    ::::::::
Db   1353 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1412

Qy   1341 tcctataagggtcacctct 1359
          :::: :     :: :::::
Db   1413 YYYYYYYYYYYYYYYYYYY 1431



Search completed: August 19, 2002, 18:12:40
Job time: 11393 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 15:00:57 ; Search time 1589.67 Seconds
(without alignments)
15393.119 Million cell updates/sec

Title: US-09-902-759-38
Perfect score: 1813
Sequence: 1 ggagccgccctgggtgtcag.....cataatgtttgtatgaaaaa 1813

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match	Length	DB	ID	Description	
c	1	1026.2	56.6	1069	9	AL573851	AL573851	AL573851
	2	1005.6	55.5	1017	9	AL547358	AL547358	AL547358
	3	992.4	54.7	1045	9	AL513572	AL513572	AL513572
c	4	947.6	52.3	986	9	AL573030	AL573030	AL573030
	5	947.6	52.3	1013	9	AL550211	AL550211	AL550211
	6	942.6	52.0	1003	9	AL552901	AL552901	AL552901
c	7	942	52.0	955	9	AL571713	AL571713	AL571713
c	8	937.2	51.7	1026	9	AL573957	AL573957	AL573957
	9	911.6	50.3	969	9	AL548482	AL548482	AL548482
	10	911	50.2	1109	9	AL549789	AL549789	AL549789
c	11	910.2	50.2	998	9	AL572321	AL572321	AL572321
	12	906.6	50.0	973	9	AL549049	AL549049	AL549049
c	13	896	49.4	978	9	AL576327	AL576327	AL576327
	14	895.8	49.4	938	9	AL546335	AL546335	AL546335
	15	895.8	49.4	999	9	AL554790	AL554790	AL554790
c	16	893.6	49.3	938	9	AL574910	AL574910	AL574910
c	17	890.6	49.1	999	9	AL577433	AL577433	AL577433
	18	886.2	48.9	920	9	AL553280	AL553280	AL553280
	19	883.6	48.7	946	9	AL551281	AL551281	AL551281
	20	863.6	47.6	894	9	AL537139	AL537139	AL537139
	21	843.6	46.5	1816	11	AK009223	AK009223 Mus muscu	
	22	842.8	46.5	907	9	AL549957	AL549957	AL549957
	23	842.4	46.5	1859	11	BC019460	BC019460 Mus muscu	
	24	830.6	45.8	900	9	AL550946	AL550946	AL550946
	25	819.4	45.2	853	10	BI771838	BI771838 603055231	
	26	809.8	44.7	853	9	AL555047	AL555047	AL555047
	27	806.8	44.5	834	10	BI769077	BI769077 603057054	
	28	798	44.0	878	9	AL549197	AL549197	AL549197
c	29	787.6	43.4	886	9	AL550912	AL550912	AL550912
	30	784.8	43.3	790	9	AL551438	AL551438	AL551438
	31	777	42.9	885	10	BI767362	BI767362 603057503	
	32	766	42.3	789	10	BI821049	BI821049 603035511	
c	33	764.4	42.2	795	9	AL577654	AL577654	AL577654
	34	758.2	41.8	872	10	BI819730	BI819730 603041421	
	35	737.8	40.7	754	10	BI771884	BI771884 603055290	
	36	726.2	40.1	774	10	BI916766	BI916766 603178773	
	37	723.6	39.9	735	9	AL547289	AL547289	AL547289
	38	723.6	39.9	833	10	BI759939	BI759939 603044368	
	39	718	39.6	905	10	BI818810	BI818810 603037664	
c	40	710	39.2	739	9	AL566674	AL566674	AL566674
	41	707.4	39.0	753	10	BI772732	BI772732 603053265	
	42	703.8	38.8	760	10	BG759963	BG759963 602733576	
	43	699.8	38.6	782	10	BI909870	BI909870 603070501	
	44	690.4	38.1	748	10	BG758052	BG758052 602712209	
	45	666.2	36.7	861	10	BI517736	BI517736	

ALIGNMENTS

```
RESULT   1
AL573851/c
LOCUS       AL573851                1069 bp     mRNA     linear    EST
16-FEB-2001
DEFINITION  AL573851 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI054YI01 3
            prime, mRNA sequence.
ACCESSION   AL573851
VERSION     AL573851.1  GI:12933489
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1069)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .1069
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI054YI01"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer.  Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      248 a    269 c    327 g    224 t      1 others
ORIGIN
```

Query Match 56.6%; Score 1026.2; DB 9; Length 1069;
Best Local Similarity 99.5%; Pred. No. 2.7e-232;
Matches 1050; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

```
Qy     714 ttctttgcaccagcattagatgtcatccgtgggtctttaagcctcaccaacctttcgtct 773
           ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1061 TTTCTTGCACCAGCATTAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCT 1002

Qy     774 tccatggctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaatgtaat 833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1001 TCCATGGCTGGAGTCTATGTCTGCAAGGCCCACAATGAGGT-GGCACTGCCCAATGTAAT 943

Qy     834 gtgacgctggaagtgagcacagggcctggagctgcagtggttgctggagctgttgtgggt 893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     942 GTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGT 883

Qy     894 accctggttggactggggttgctggctgggctggtcctcttgtaccaccgccggggcaag 953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     882 ACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAG 823

Qy     954 gccctggaggagccagccaatgatatcaaggaggatgccattgctccccggaccctgccc 1013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     822 GCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCC 763

Qy    1014 tggcccaagagctcagacacaatctccaagaatgggacccttcctctgtcacctccgca 1073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     762 TGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTCACCTCCGCA 703

Qy    1074 cgagccctccggccaccccatggccctcccaggcctggtgcattgaccccccacgcccagt 1133
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     702 CGAG-CCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGT 644

Qy    1134 ctctccagccaggccctgccctcaccaagactgcccacgacagatggggcccaccctcaa 1193
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     643 CTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCAA 584

Qy    1194 ccaatatcccccatccctggtggggtttcttcctctggcttgagccgcatgggtgctgtg 1253
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     583 CCAATATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTG 524

Qy    1254 cctgtgatggtgcctgcccagagtcaagctggctctctggtatgatgaccccaccactca 1313
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     523 CCTGTGATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCA 464

Qy    1314 ttggctaaaggatttggggtctctccttcctataagggtcacctctagcacagaggcctg 1373
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     463 TTGGCTAAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTG 404

Qy    1374 agtcatgggaaagagtcacactcctgacccttagtactctgcccccacctctctttactg 1433
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     403 AGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCCACCTCTCTTTACTG 344

Qy    1434 tgggaaaaccatctcagtaagacctaagtgtccaggagacagaaggagaagaggaagtgg 1493
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     343 TGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGG 284

Qy    1494 atctggaattgggaggagcctccacccacccctgactcctccttatgaagccagctgctg 1553
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     283 ATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTG 224

Qy    1554 aaattagctactcaccaagagtgaggggcagagacttccagtcactgagtctcccaggcc 1613
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     223 AAATTAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCC 164

Qy    1614 cccttgatctgtaccccaccctatctaacaccacccttggctcccactccagctccctg 1673
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     163 CCCTTGATCTGTACCCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTG 104
```

```
Qy   1674 tattgatataacctgtcaggctggcttggttaggttttactggggcagaggatagggaat 1733
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    103 TATTGATATAACCTGTTAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAAT 44

Qy   1734 ctcttattaaaactaacatgaaatatgtgttgttt 1768
          |||||||||||||||||||||||||||||||||||
Db     43 CTCTTATTAAAACTAACATGAAATATGTGTTGTTT 9


RESULT   2
AL547358
LOCUS         AL547358                  1017 bp     mRNA     linear    EST
16-FEB-2001
DEFINITION  AL547358 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI007YN05 5
            prime, mRNA sequence.
ACCESSION   AL547358
VERSION     AL547358.1  GI:12881364
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1017)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .1017
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI007YN05"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer.  Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      185 a    311 c    305 g    215 t      1 others
ORIGIN


  Query Match             55.5%;  Score 1005.6;  DB 9;  Length 1017;
  Best Local Similarity   99.8%;  Pred. No. 2e-227;
  Matches 1016;  Conservative    1;  Mismatches    0;  Indels    1;  Gaps
1;

Qy     13 ggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcctcggcacctgcag 72
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||

Db      1 GGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAG-CTCGGCACCTGCAG 59

Qy     73 gtccgtgcgtcccgcggctggcgcccctgactccgtcccggccagggagggccatgattt 132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 GTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGCCATGATTT 119

Qy    133 ccctcccggggcccctggtgaccaacttgctgcggtttttgttcctggggctgagtgccc 192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 CCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGAGTGCCC 179

Qy    193 tcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaaccggttgcaggcgg 252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 TCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGGCGG 239

Qy    253 tggagggaggggaagtggtgcttccagcgtggtacaccttgcacggggaggtgtcttcat 312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 TGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTGTCTTCAT 299

Qy    313 cccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaagaaaaggaggatc 372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 CCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC 359

Qy    373 aggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtatccttggtctact 432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 AGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACT 419

Qy    433 ccatgccctcccggaacctgtccctgcggctggagggtctccaggagaaagactctggcc 492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 CCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCC 479

Qy    493 cctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggggccacagcatca 552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 CCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCA 539

Qy    553 aaaccttagaactcaatgtactggttcctccagctcctccatcctgccgtctccagggtg 612
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 AAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTG 599

Qy    613 tgccccatgtgggggcaaacgtgaccctgagctgccagtctccaaggagtaagcccgctg 672
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 TGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTG 659

Qy    673 tccaataccagtgggatcggcagcttccatccttccagactttctttgcaccagcattag 732
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 TCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAG 719

Qy    733 atgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatggctggagtctatg 792
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 ATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATG 779

Qy    793 tctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgctggaagtgagca 852
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 TCTGCAAGGCCCACAATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCA 839

Qy    853 cagggcctggagctgcagtggttgctggagctgttgtgggtaccctggttggactggggt 912
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    840 CAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGT 899
```

```
Qy    913 tgctggctgggctggtcctcttgtaccaccgccggggcaaggccctggaggagccagcca 972
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    900 TGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCA 959

Qy    973 atgatatcaaggaggatgccattgctccccggaccctgccctggcccaagagctcaga 1030
          ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db    960 ATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGSCCAAGAGCTCAGA 1017


RESULT   3
AL513572
LOCUS         AL513572                  1045 bp     mRNA     linear    EST
13-FEB-2001
DEFINITION  AL513572 LTI_NFL006_PL2 Homo sapiens cDNA clone XCL0BA001ZD03 5
            prime, mRNA sequence.
ACCESSION   AL513572
VERSION     AL513572.1  GI:12777066
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1045)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .1045
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="XCL0BA001ZD03"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer.  Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      196 a    304 c    302 g    229 t     14 others
ORIGIN


  Query Match             54.7%;  Score 992.4;  DB 9;  Length 1045;
  Best Local Similarity   97.0%;  Pred. No. 2.7e-224;
  Matches 1015;  Conservative   14;  Mismatches   15;  Indels    2;  Gaps
2;

Qy     11 tgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcctcggcacctgc 70
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||

Db      1 TGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCA-CCTCGGCACCTGC 59

Qy     71 aggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccagggagggccatgat 130
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 AGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGCCATGAT 119

Qy    131 ttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctggggctgagtgc 190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 TTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGAGTGC 179

Qy    191 cctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaaccggttgcaggc 250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 CCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGGC 239

Qy    251 ggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacggggaggtgtcttc 310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 GGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTGTCTTC 299

Qy    311 atcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaagaaaaggagga 370
          ||||||||:|||||||||||||||||||||||||||||||:|:|||:|||||||||||
Db    300 ATCCCAGCMATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAAMARAAARAAAAGGAGGA 359

Qy    371 tcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtatccttggtcta 430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 TCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTA 419

Qy    431 ctccatgccctcccggaacctgtccctgcggctggagggtctccaggagaaagactctgg 490
          |||||||||||||||||||| ||||||||||||||||||||||||||:|||||||
Db    420 CTCCATGCCCTCCCGGAACCTGTTCCTGCGGCTGGAGGGTCTCCAGGAGAAARACTCTGG 479

Qy    491 cccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggggccacagcat 550
          |||||||||||||||||||| ||||| | ||||||||||||:|||||||||||||||
Db    480 CCCCTACAGCTGCTCCGTGAATTTGCAAAAAAAACAAGGCAAATMTAGGGGCCACAGCAT 539

Qy    551 caaaaccttagaactcaatgtactggttcctccagctcctccatcctgccgtctccaggg 610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 CAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGG 599

Qy    611 tgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaaggagtaagcccgc 670
          |||||||||||||||||||||||||||||||||||||||| |||||||||:|||||||
Db    600 TGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTTTCCAAGGAGTWAGCCCGC 659

Qy    671 tgtccaataccagtgggatcggcagcttccatccttccagactttctttgcaccagcatt 730
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 TGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATT 719

Qy    731 agatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatggctggagtcta 790
          ||||||:|||||||||| ||||||||||||||||||||||||||||||||||:||
Db    720 AGATGTYATCCGTGGGTTTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTYTA 779

Qy    791 tgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgctggaagtgag 850
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 TGTTTGCAAGGCCCACAATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAG 839

Qy    851 cacagggcctggagctgcagtggttgctggagctgttgtgggtaccctggttggactggg 910
          |||||||||||||||||||| |||||||||||||||||||| ||||||||||||||||
Db    840 CACAGGGCCTGGAGCTGCAGTTGTTGCTGGAGCTGTTGTGGGTA-CCTGGTTGGACTGGG 898
```

```
Qy     911 gttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctggaggagccagc 970
           ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db     899 GTTGCTGGCTGGGCTGGTCCTCTTGTACCAMCGCCGGGGCAAGGCCCTGGAGGAGCCAGC 958

Qy     971 caatgatatcaaggaggatgccattgctccccggaccctgccctggcccaagagctcaga 1030
           :|||||:||:|||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     959 MAATGAWATMAAGGAGGATGCCATTTCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGA 1018

Qy    1031 cacaatctccaagaatgggacccttt 1056
           | |||:||||||||| ||  || ||
Db    1019 AAAAATYTCCAAGAATTGGGACCCTT 1044


RESULT   4
AL573030/c
LOCUS         AL573030                  986 bp     mRNA     linear    EST
16-FEB-2001
DEFINITION  AL573030 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI014YD08 3
            prime, mRNA sequence.
ACCESSION   AL573030
VERSION     AL573030.1  GI:12931874
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 986)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .986
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI014YD08"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer.  Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      212 a    250 c    302 g    210 t     12 others
ORIGIN


  Query Match             52.3%;  Score 947.6;  DB 9;  Length 986;
  Best Local Similarity   98.1%;  Pred. No. 1.1e-213;
  Matches  969;  Conservative    9;  Mismatches    8;  Indels    2;  Gaps
```

```
2;

Qy     793 tctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgctggaagtgagca 852
           |||||||||||||||||||| :|||||||||||||||||||||||||||||||||||||||
Db     986 TCTGCAAGGCCCACAATGAGG-KGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCA 928

Qy     853 cagggcctggagctgcagtggttgctggagctgttgtgggtaccctggttggactggggt 912
           |||||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||
Db     927 CAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGATGT-GGTACCCTGGTTGGACTGGGGT 869

Qy     913 tgctggctgggctggtcctcttgtaccaccgccggggcaaggccctggaggagccagcca 972
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     868 GGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCA 809

Qy     973 atgatatcaaggaggatgccattgctccccggaccctgccctggcccaagagctcagaca 1032
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     808 ATGATATCAAGGAGGATGCCATTGCTCCCCGGACCCTACCCTGGCCCAAGAGCTCAGACA 749

Qy    1033 caatctccaagaatgggacccttttcctctgtcacctccgcacgagccctccggccacccc 1092
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     748 CAATCTCCAAGAATGGGACCCTTTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCC 689

Qy    1093 atggccctcccaggcctggtgcattgacccccacgcccagtctctccagccaggccctgc 1152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     688 ATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGC 629

Qy    1153 cctcaccaagactgcccacgacagatggggcccaccctcaaccaatatcccccatccctg 1212
           ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db     628 CCTCACCAAGACTGCCCACGACAGATGGGGCCCACCCTCMACCAATATCCCCCATCCCTG 569

Qy    1213 gtggggtttcttcctctggcttgagccgcatgggtgctgtgcctgtgatggtgcctgccc 1272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db     568 GTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGATGGTGCCTGCCM 509

Qy    1273 agagtcaagctggctctctggtatgatgaccccaccactcattggctaaaggatttgggg 1332
           ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db     508 AGAGTCAAGCTGGCTCTCTGGTATGATGACCCCACCACTCWTTGGCTAAAGGATTTGGGG 449

Qy    1333 tctctccttcctataagggtcacctctagcacagaggcctgagtcatgggaaagagtcac 1392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 TCTCTCCTTCCTATAAGGGTCACCTCTAGCACAGAGGCCTGAGTCATGGGAAAGAGTCAC 389

Qy    1393 actcctgacccttagtactctgcccccacctctctttactgtgggaaaaccatctcagta 1452
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 ACTCCTGACCCTTAGTACTCTGCCCCCACCTCTCTTTACTGTGGGAAAACCATCTCAGTA 329

Qy    1453 agacctaagtgtccaggagacagaaggagaagaggaagtggatctggaattgggaggagc 1512
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db     328 AGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATTGGGAGGARC 269

Qy    1513 ctccacccaccccctgactcctccttatgaagccagctgctgaaattagctactcaccaag 1572
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     268 CTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTACTCACCAAG 209

Qy    1573 agtgaggggcagagacttccagtcactgagtctcccaggccccccttgatctgtaccccac 1632
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 AGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGATCTGTACCCCAC 149
```

```
Qy    1633 ccctatctaacaccacccttggctcccactccagctccctgtattgatataacctgtcag 1692
           |||||||||||||||||  :|||||||| || || ||::||||||||||||||||||||
Db     148 CCCTATCTAACACCACCCAYGGCTCCCACSCCSGCSCCSKGTATTGATATAACCTGTCAG 89

Qy    1693 gctggcttggttaggttttactggggcagaggataggg-aatctcttattaaaactaacat 1752
           ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db      88 GCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTATTAAAACTAACAT 29

Qy    1753 gaaatatgtgttgttttcatttgcaaat 1780
           |||||||||||||||||| ||||||:
Db      28 GAAATATGTGTTGTTTTCATATGCAAAW 1
```

RESULT 5
AL550211
LOCUS AL550211 1013 bp mRNA linear EST
16-FEB-2001
DEFINITION AL550211 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI039YD07 5 prime, mRNA sequence.
ACCESSION AL550211
VERSION AL550211.1 GI:12886963
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1013)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES Location/Qualifiers
source 1. .1013
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI039YD07"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 183 a 309 c 304 g 216 t 1 others
ORIGIN

Query Match 52.3%; Score 947.6; DB 9; Length 1013;
Best Local Similarity 99.3%; Pred. No. 1.1e-213;
Matches 1003; Conservative 1; Mismatches 0; Indels 6; Gaps

```
Qy    1793 5;

Qy      11 tgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcctcggcacctgc 70
           |||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db       1 TGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGC--CCTCGGCACCTGC 58

Qy      71 aggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccagggagggccatgat 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      59 AGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGCCATGAT 118

Qy     131 ttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctggggctgagtgc 190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     119 TTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGAGTGC 178

Qy     191 cctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaaccggttgcaggc 250
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     179 CCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGGC 238

Qy     251 ggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacggggaggtgtcttc 310
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     239 GGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTGTCTTC 298

Qy     311 atcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaagaaaaggagga 370
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     299 ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGA 358

Qy     371 tcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtatccttggtcta 430
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     359 TCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTA 418

Qy     431 ctccatgccctcccggaacctgtccctgcggctggagggtctccaggagaaagactctgg 490
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     419 CTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGG 478

Qy     491 cccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggggccacagcat 550
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     479 CCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCAT 538

Qy     551 caaaaccttagaactcaatgtactggttcctccagctcctccatcctgccgtctccaggg 610
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     539 CAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGG 598

Qy     611 tgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaaggagtaagcccgc 670
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     599 TGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGC 658

Qy     671 tgtccaataccagtgggatcggcagcttccatccttccagactttctttgcaccagcatt 730
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     659 TGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATT 718

Qy     731 agatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatggctggagtcta 790
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     719 AGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTA 778

Qy     791 tgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgctggaagtgag 850
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     779 TGTCTGCAAGGCCCACAATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAG 838
```

```
Qy    851 cacagggcctggagctgcagtggttgctggagctgttgtgggtaccctggttggactggg 910
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    839 CACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTA-CCTGGTTGGACTGGG 897

Qy    911 gttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctggaggagccagc 970
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    898 GTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGG-CCTGGAGGAGCCAG- 955

Qy    971 caatgatatcaaggaggatgccattgctccccggaccctgccctggccca 1020
          |:||||||||||||||||||||||||| ||||||||||||||||||||
Db    956 CMATGATATCAAGGAGGATGCCATTGCT-CCCGGACCCTGCCCTGGCCCA 1004


RESULT   6
AL552901
LOCUS        AL552901                1003 bp     mRNA     linear    EST
16-FEB-2001
DEFINITION  AL552901 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI071YE19 5
            prime, mRNA sequence.
ACCESSION   AL552901
VERSION     AL552901.1  GI:12892228
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1003)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .1003
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI071YE19"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer.  Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      183 a    304 c    301 g    213 t      2 others
ORIGIN


  Query Match             52.0%;  Score 942.6;  DB 9;  Length 1003;
  Best Local Similarity   99.6%;  Pred. No. 1.7e-212;
  Matches  975;  Conservative    1;  Mismatches    0;  Indels    3;  Gaps
```

```
3;

Qy     13 ggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcctcggcacctgcag 72
          |||||||||||||||||||||||||||||||||||||||||||||||||| :|||||||||||||
Db      1 GGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCA-SCTCGGCACCTGCAG 59

Qy     73 gtccgtgcgtcccgcggctggcgcccctgactccgtcccggccagggagggccatgattt 132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 GTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGCCATGATTT 119

Qy    133 ccctcccggggcccctggtgaccaacttgctgcggtttttgttcctggggctgagtgccc 192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 CCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGAGTGCCC 179

Qy    193 tcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaaccggttgcaggcgg 252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 TCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGGCGG 239

Qy    253 tggagggagggaagtggtgcttccagcgtggtacaccttgcacggggaggtgtcttcat 312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 TGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTGTCTTCAT 299

Qy    313 cccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaagaaaaggaggatc 372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 CCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC 359

Qy    373 aggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtatccttggtctact 432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 AGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACT 419

Qy    433 ccatgccctcccggaacctgtccctgcggctggagggtctccaggagaaagactctggcc 492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 CCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCC 479

Qy    493 cctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggggccacagcatca 552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 CCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCA 539

Qy    553 aaaccttagaactcaatgtactggttcctccagctcctccatcctgccgtctccagggtg 612
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 AAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTG 599

Qy    613 tgccccatgtgggggcaaacgtgaccctgagctgccagtctccaaggagtaagcccgctg 672
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 TGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTG 659

Qy    673 tccaataccagtgggatcggcagcttccatccttccagactttctttgcaccagcattag 732
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 TCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAG 719

Qy    733 atgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatggctggagtctatg 792
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 ATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATG 779

Qy    793 tctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgctggaagtgagca 852
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 TCTGCAAGGCCCACAATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCA 839
```

```
Qy     853 cagggcctggagctgcagtggttgctggagctgttgtgggtaccctggttggactggggt 912
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 CAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGT 899

Qy     913 tgctggctgggctggtcctcttgtaccaccgccggggcaaggccctggaggagccagcca 972
           ||||||||||||||| ||||||||||||||||||||||||||||||||| ||||||
Db     900 TGCTGGCTGGGCTGGT-CTCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAG-CAGCCA 957

Qy     973 atgatatcaaggaggatgc 991
           ||||||||||||||||||||
Db     958 ATGATATCAAGGAGGATGC 976


RESULT   7
AL571713/c
LOCUS         AL571713                955 bp     mRNA     linear    EST
16-FEB-2001
DEFINITION  AL571713 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI031YI09 3
            prime, mRNA sequence.
ACCESSION   AL571713
VERSION     AL571713.1  GI:12929283
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 955)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .955
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI031YI09"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer.  Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      207 a    247 c    300 g    200 t      1 others
ORIGIN


  Query Match             52.0%;  Score 942;  DB 9;  Length 955;
  Best Local Similarity   99.7%;  Pred. No. 2.3e-212;
  Matches  953;  Conservative    1;  Mismatches    1;  Indels    1;  Gaps
```

```
1;

Qy     798 aaggcccacaatgaggtgggcactgcccaatgtaatgtgacgctggaagtgagcacaggg 857
           |||||||||||||||| |||||:||||||||||||||||||||||||||||||||||||
Db     955 AAGGCCCACAATGAGGT-GGCACTSCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGG 897

Qy     858 cctggagctgcagtggttgctggagctgttgtgggtaccctggttggactggggttgctg 917
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     896 CCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTG 837

Qy     918 gctgggctggtcctcttgtaccaccgccggggcaaggccctggaggagccagccaatgat 977
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     836 GCTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGAT 777

Qy     978 atcaaggaggatgccattgctccccggaccctgccctggcccaagagctcagacacaatc 1037
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     776 ATCAAGGAGGATGCCATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATC 717

Qy    1038 tccaagaatgggacccttttcctctgtcacctccgcacgagccctccggccaccccatggc 1097
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     716 TCCAAGAATGGGACCCTTTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCCATGGC 657

Qy    1098 cctcccaggcctggtgcattgaccccacgcccagtctctccagccaggccctgccctca 1157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     656 CCTCCCAGGCCTGGTGCATTGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCA 597

Qy    1158 ccaagactgcccacgacagatggggcccaccctcaaccaatatcccccatccctggtggg 1217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     596 CCAAGACTGCCCACGACAGATGGGGCCCACCCTCAACCAATATCCCCCATCCCTGGTGGG 537

Qy    1218 gtttcttcctctggcttgagccgcatgggtgctgtgcctgtgatggtgcctgcccagagt 1277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     536 GTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTGTGATGGTGCCTGCCCAGAGT 477

Qy    1278 caagctggctctctggtatgatgaccccaccactcattggctaaaggatttggggtctct 1337
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     476 CAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTAAAGGATTTGGGGTCTCT 417

Qy    1338 ccttcctataagggtcacctctagcacagaggcctgagtcatgggaaagagtcacactcc 1397
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     416 CCTTCCTATAGGGGTCACCTCTAGCACAGAGGCCTGAGTCATGGGAAAGAGTCACACTCC 357

Qy    1398 tgacccttagtactctgccccccacctctctttactgtgggaaaaccatctcagtaagacc 1457
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     356 TGACCCTTAGTACTCTGCCCCCACCTCTCTTTACTGTGGGAAAACCATCTCAGTAAGACC 297

Qy    1458 taagtgtccaggagacagaaggagaagaggaagtggatctggaattgggaggagcctcca 1517
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     296 TAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATTGGGAGGAGCCTCCA 237

Qy    1518 cccacccctgactcctccttatgaagccagctgctgaaattagctactcaccaagagtga 1577
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     236 CCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTACTCACCAAGAGTGA 177

Qy    1578 ggggcagagacttccagtcactgagtctcccaggcccccttgatctgtaccccacccctа 1637
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     176 GGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGCCCCCTTGATCTGTACCCCACCCCTA 117
```

```
Qy   1638 tctaacaccacccttggctcccactccagctccctgtattgatataacctgtcaggctgg 1697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    116 TCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGG 57

Qy   1698 cttggttaggttttactggggcagaggatagggaatctcttattaaaactaacatg 1753
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     56 CTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTATTAAAACTAACATG 1
```

```
RESULT   8
AL573957/c
LOCUS         AL573957                1026 bp     mRNA     linear    EST
16-FEB-2001
DEFINITION  AL573957 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI053YD20 3
            prime, mRNA sequence.
ACCESSION   AL573957
VERSION     AL573957.1  GI:12933695
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1026)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .1026
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI053YD20"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer.  Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      238 a    249 c    317 g    218 t      4 others
ORIGIN
```

```
  Query Match             51.7%;  Score 937.2;  DB 9;  Length 1026;
  Best Local Similarity   97.7%;  Pred. No. 3.2e-211;
  Matches 1010;  Conservative    4;  Mismatches   12;  Indels    8;  Gaps
6;

Qy    751 taagcctcaccaacctttcgtcttccatggctggagtctatgtctgcaaggcccacaatg 810
          | | ||||||||||||||| : | |        |||||||||||||||| ||||||||||
```

```
Db   1026 TTAACCTCACCAACCTTTCTYTTCC---ATGCTGAGTCTATGTCTGCAA-GCCCACAATG 971

Qy    811 aggtgggcactgcccaatgtaatgtgacgctggaagtgagcacagggcctggagctgcag 870
          |||| |||||| |||||||||||||||||| |||:|||||||| ||||||||||||||
Db    970 AGGT-GGCACTCCCCAATGTAATGTGACGCT-GAARTGAGCACA-GGCCTGGAGCTGCAG 914

Qy    871 tggttgctggagctgttgtgggtaccctggttggactggggttgctggctgggctggtcc 930
          ||||||||||:|||||||| |||||||||||| ||||||||||||||||||||||||||
Db    913 TGGTTGCTGGMGCTGTTGT-GGTACCCTGGTTGAACTGGGGTTGCTGGCTGGGCTGGTCC 855

Qy    931 tcttgtaccaccgccggggcaaggccctggaggagccagccaatgatatcaaggaggatg 990
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    854 TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATG 795

Qy    991 ccattgctccccggaccctgccctggcccaagagctcagacacaatctccaagaatggga 1050
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    794 CCATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGA 735

Qy   1051 cccttcctctgtcacctccgcacgagccctccggccaccccatggccctcccaggcctg 1110
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    734 CCCTTTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTG 675

Qy   1111 gtgcattgaccccacgcccagtctctccagccaggccctgccctcaccaagactgccca 1170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    674 GTGCATTGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCCA 615

Qy   1171 cgacagatggggcccaccctcaaccaatatccccccatccctggtggggtttcttcctctg 1230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    614 CGACAGATGGGGCCCACCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCCTCTG 555

Qy   1231 gcttgagccgcatgggtgctgtgcctgtgatggtgcctgcccagagtcaagctggctctc 1290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    554 GCTTGAGCCGCATGGGTGCTGTGCCTGTGATGGTGCCTGCCCAGAGTCAAGCTGGCTCTC 495

Qy   1291 tggtatgatgaccccaccactcattggctaaaggatttggggtctctccttcctataagg 1350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    494 TGGTATGATGACCCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCCTATAAGG 435

Qy   1351 gtcacctctagcacagaggcctgagtcatgggaaagagtcacactcctgacccttagtac 1410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    434 GTCACCTCTAGCACAGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTAC 375

Qy   1411 tctgcccccacctctctttactgtgggaaaaccatctcagtaagacctaagtgtccagga 1470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 TCTGCCCCCACCTCTCTTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGA 315

Qy   1471 gacagaaggagaagaggaagtggatctggaattgggaggagcctccacccacccctgact 1530
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 GACAGAAGGAGAAGAGGAAGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACT 255

Qy   1531 cctccttatgaagccagctgctgaaattagctactcaccaagagtgaggggcagagactt 1590
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 CCTCCTTATGAAGCCAGCTGCTGAAATTAGCTACTCACCAAGAGTGAGGGGCAGAGACTT 195

Qy   1591 ccagtcactgagtctcccaggcccccttgatctgtaccccacccctatctaacaccaccc 1650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 CCAGTCACTGAGTCTCCCAGGCCCCCTTGATCTGTACCCCACCCCTATCTAACACCACCC 135
```

```
Qy   1651 ttggctcccactccagctccctgtattgatataacctgtcaggctggcttggttaggttt 1710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 TTGGCTCCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTT 75

Qy   1711 tactggggcagaggatagggaatctcttattaaaactaacatgaaatatgtgttgttttc 1770
          ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db     74 TACTGGGGCAGAGGATAGGGAATCTCTTATTAAAACTMACATGAAATATGTGTTGTTTTC 15

Qy   1771 atttgcaaatttaa 1784
          ||||||||||||||
Db     14 ATTTGCAAATTTAA 1
```

RESULT 9
AL548482
LOCUS AL548482 969 bp mRNA linear EST
16-FEB-2001
DEFINITION AL548482 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI014YD08 5 prime, mRNA sequence.
ACCESSION AL548482
VERSION AL548482.1 GI:12883529
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 969)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES Location/Qualifiers
source 1. .969
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI014YD08"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 177 a 289 c 293 g 208 t 2 others
ORIGIN

Query Match 50.3%; Score 911.6; DB 9; Length 969;
Best Local Similarity 98.6%; Pred. No. 3.7e-205;
Matches 960; Conservative 2; Mismatches 7; Indels 5; Gaps 4;

```
Qy     12 gggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcctcggcacctgca 71
          ||||||||||||||||||||||||||||||||||||||||||||:| ||||||||||||
Db      1 GGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCMG-CTCGGCACCTGCA 59

Qy     72 ggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccagggagggccatgatt 131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 GGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGCCATGATT 119

Qy    132 tccctcccggggcccctggtgaccaacttgctgcggtttttgttcctggggctgagtgcc 191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 TCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGAGTGCC 179

Qy    192 ctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaaccggttgcaggcg 251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 CTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGGCG 239

Qy    252 gtggagggaggggaagtggtgcttccagcgtggtacaccttgcacggggaggtgtcttca 311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 GTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTGTCTTCA 299

Qy    312 tcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaagaaaaggaggat 371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 TCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGAT 359

Qy    372 caggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtatccttggtctac 431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 CAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTAC 419

Qy    432 tccatgccctcccggaacctgtccctgcggctggagggtctccaggagaaagactctggc 491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 TCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGC 479

Qy    492 ccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggggccacagcatc 551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 CCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATC 539

Qy    552 aaaaccttagaactcaatgtactggttcctccagctcctccatcctgccgtctccagggt 611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 AAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGT 599

Qy    612 gtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaaggagtaagcccgct 671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 GTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCT 659

Qy    672 gtccaataccagtgggatcggcagcttccatccttccagactttctttgcaccagcatta 731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 GTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTA 719

Qy    732 gatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatggctggagtctat 791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 GATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTAT 779

Qy    792 gtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgctggaagtgagc 851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 GTCTGCAAGGCCCACAATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGC 839
```

```
Qy    852 acagggcctggagctgcagtggttgctggagctgttgtgggtaccctggttggactgggg 911
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    840 ACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTA-CCTGGTTGGACTGGGG 898

Qy    912 ttgctggctgggctggtcctcttgtaccaccgccggggcaaggccctggaggagccagcc 971
          |||||||||||||||||||||||| ||||||||||||||||||   |  |   || ||
Db    899 TTGCTGGCTGGGCTGGTCCTCTTGTA-CACCGCCGGGGCAAGGCC--TGGAGGAGCAACC 955

Qy    972 aatgatatcaagga 985
          ||||||||:|||||
Db    956 AATGATATHAAGGA 969
```

```
RESULT  10
AL549789
LOCUS         AL549789                  1109 bp     mRNA     linear    EST
16-FEB-2001
DEFINITION  AL549789 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI054YI01 5
            prime, mRNA sequence.
ACCESSION   AL549789
VERSION     AL549789.1  GI:12886119
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1109)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .1109
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI054YI01"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer.  Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      204 a    337 c    327 g    238 t      3 others
ORIGIN
```

```
  Query Match             50.2%;  Score 911;  DB 9;  Length 1109;
  Best Local Similarity   98.9%;  Pred. No. 5.4e-205;
  Matches  937;  Conservative    1;  Mismatches    6;  Indels    3;  Gaps
```

```
2;

Qy     10 ctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcctcggcacctg 69
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| :||||||||||
Db      1 CTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCA-SCTCGGCACCTG 59

Qy     70 caggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccagggagggccatga 129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 CAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGCCATGA 119

Qy    130 tttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctggggctgagtg 189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 TTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGAGTG 179

Qy    190 ccctcgcgcccccctcgcgggcccagctgcaactgcacttgcccgccaaccggttgcagg 249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 CCCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGG 239

Qy    250 cggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacggggaggtgtctt 309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 CGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTGTCTT 299

Qy    310 catcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaagaaaaggagg 369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 CATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGG 359

Qy    370 atcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtatccttggtct 429
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 ATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCT 419

Qy    430 actccatgccctcccggaacctgtccctgcggctggagggtctccaggagaaagactctg 489
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 ACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTG 479

Qy    490 gcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggggccacagca 549
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 GCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCA 539

Qy    550 tcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgccgtctccagg 609
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 TCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGG 599

Qy    610 gtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaaggagtaagcccg 669
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 GTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCG 659

Qy    670 ctgtccaataccagtgggatcggcagcttccatccttccagactttctttgcaccagcat 729
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 CTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCAT 719

Qy    730 tagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatggctggagtct 789
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 TAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCT 779

Qy    790 atgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgctggaagtga 849
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 ATGTCTGCAAGGCCCACAATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGA 839
```

```
Qy    850 gcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctggttggactgg 909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    840 GCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGG 899

Qy    910 ggttgctggctgggctggtcctcttgtaccaccgccggggcaaggcc 956
          ||||||||||||||||||    |    ||||||||||||||||||
Db    900 GGTTGCTGGCTGGGCTGGTC--TCTTGTACACCGCCGGGGCAAGGCC 944


RESULT  11
AL572321/c
LOCUS         AL572321                998 bp     mRNA     linear    EST
16-FEB-2001
DEFINITION  AL572321 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI007YN05 3
            prime, mRNA sequence.
ACCESSION   AL572321
VERSION     AL572321.1  GI:12930475
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 998)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .998
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI007YN05"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer.  Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      220 a    253 c    312 g    206 t      7 others
ORIGIN


  Query Match             50.2%;  Score 910.2;  DB 9;  Length 998;
  Best Local Similarity   97.7%;  Pred. No. 8e-205;
  Matches  980;  Conservative    6;  Mismatches    9;  Indels    8;  Gaps
6;

Qy    768 tcgtcttccatggctggagtctatgtctgcaaggcccacaatgaggtgggcactgcccaa 827
          |||||||:|||||||||||||||||||||||||||||||||||||||| ||||||||||||
```

```
Db    998 TCGTCTYCCATGGCTGGAGTCTATGTCTGCAAGGCCCACAATGAGGT-GGCACTGCCCAA 940

Qy    828 tgtaatgtgacgctggaagtgagcacagggcctggagctgcagtggttgctggagctgtt 887
          ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db    939 TGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTKGCTGGAGCTGTT 880

Qy    888 gtgggtaccctggttggactggggttgctggctgggctggtcctcttgtaccaccgccgg 947
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    879 GTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCCTCTTGTACCACCGCCGG 820

Qy    948 ggcaaggccctggaggagccagccaatgatatcaaggaggatgccattgctccccggacc 1007
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    819 GGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCCATTGCTCCCCGGACC 760

Qy   1008 ctgccctggcccaagagctcagacacaatctccaagaatgggacccttttcctctgtcacc 1067
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    759 CTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCTTTCCTCTGTCACC 700

Qy   1068 tccgcacgagccctccggccaccccatggccctcccaggcctggtgcattgacccccacg 1127
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    699 TCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCATTGACCCCCACG 640

Qy   1128 cccagtctctccagccaggccctgccctcaccaagactgcccacgacagatggggcccac 1187
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    639 CCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGAT-GGGCCCAC 581

Qy   1188 cctcaaccaatatcccccatccctggtggggtttcttcctctggcttgagccgcatgggt 1247
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    580 CCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCGCATGGGT 521

Qy   1248 gctgtgcctgtgatggtgcctgcccagagtcaagctggctctctggtatgatgaccccac 1307
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    520 GCTGTGCCTGTGATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGACCCCAC 461

Qy   1308 cactcattggctaaaggatttggggtctctccttcctataagggtcacctctagcacaga 1367
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    460 CACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCCTATAGGGGTCACCTCTAGCACAGA 401

Qy   1368 ggcctgagtcatgggaaagagtcacactcctgacccttagt-actctgccccccacctctc 1426
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    400 GGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTCACTCTGCCCCCCACCTCTC 341

Qy   1427 tttactgtgggaaaaccatctcagtaagacctaagtgtccaggagacagaaggagaagag 1486
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    340 TTTACTGTGGCAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAG 281

Qy   1487 gaagtggatctggaattgggag-gagcctccacccacccctgactcctccttatgaagcc 1545
          |||||||||||||||||||||| ||:|| |||||:|||||:|||||:||||||||||||
Db    280 GAAGTGGATCTGGAATTGGGAGCGASCCCCCACCCMCCCCTSACTCCYCCTTATGAAGCC 221

Qy   1546 agctgctgaaattagctactcaccaagagtgaggggcagagacttccagtcactgagtct 1605
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    220 AGCTGCTGAAATTAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCT 161

Qy   1606 cccaggcccccttgatctgtaccccacccctatctaacaccaccccttggctcccactcca 1665
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    160 CCCAGGCCCCCTTGATCTGTACCCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCA 101
```

```
Qy   1666 gctccctgtattgatataacctgtcaggctggcttggttaggttttactggggcagagga 1725
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    100 GCTCCCTGTATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGA 41

Qy   1726 tagggaatctcttattaaaactaacatgaaatatgtgttgttt 1768
          |||| |  |   |  | |||||||||| ||||||||||||||
Db     40 TAGGAACAC---TTATTAAACTAACAT-AAATATGTGTTGTTT 2


RESULT  12
AL549049
LOCUS       AL549049                 973 bp     mRNA     linear    EST
16-FEB-2001
DEFINITION  AL549049 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI042YA17 5
            prime, mRNA sequence.
ACCESSION   AL549049
VERSION     AL549049.1  GI:12884656
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 973)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .973
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI042YA17"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer.  Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      177 a    289 c    296 g    209 t      2 others
ORIGIN


  Query Match           50.0%;  Score 906.6;  DB 9;  Length 973;
  Best Local Similarity   98.6%;  Pred. No. 5.6e-204;
  Matches  965;  Conservative    2;  Mismatches    6;  Indels    6;  Gaps
5;

Qy     13 ggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcctcggcacctgcag 72
          |||||||||||||||||||||||||||||||||||||||||||:| ||||||||||||||
```

```
Db      1 GGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCMG-CTCGGCACCTGCAG 59

Qy     73 gtccgtgcgtcccgcggctggcgcccctgactccgtcccggccagggagggccatgattt 132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 GTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGCCATGATTT 119

Qy    133 ccctcccggggcccctggtgaccaacttgctgcggtttttgttcctggggctgagtgccc 192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 CCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGAGTGCCC 179

Qy    193 tcgcgccccctcgcgggcccagctgcaactgcacttgcccgccaaccggttgcaggcgg 252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 TCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGGCGG 239

Qy    253 tggagggagggaagtggtgcttccagcgtggtacaccttgcacggggaggtgtcttcat 312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 TGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTGTCTTCAT 299

Qy    313 cccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaagaaaaggaggatc 372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 CCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC 359

Qy    373 aggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtatccttggtctact 432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 AGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACT 419

Qy    433 ccatgccctcccggaacctgtccctgcggctggagggtctccaggagaaagactctggcc 492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 CCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCC 479

Qy    493 cctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggggccacagcatca 552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 CCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCA 539

Qy    553 aaaccttagaactcaatgtactggttcctccagctcctccatcctgccgtctccagggtg 612
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 AAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTG 599

Qy    613 tgccccatgtgggggcaaacgtgaccctgagctgccagtctccaaggagtaagcccgctg 672
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 TGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTG 659

Qy    673 tccaataccagtgggatcggcagcttccatccttccagactttctttgcaccagcattag 732
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 TCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAG 719

Qy    733 atgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatggctggagtctatg 792
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 ATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATG 779

Qy    793 tctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgctggaagtgagca 852
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 TCTGCAAGGCCCACAATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCA 839

Qy    853 cagggcctggagctgcagtggttgctggagctgttgtgggtaccctggttggactggggt 912
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    840 CAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTA-CCTGGTTGGACTGGGGT 898
```

```
Qy    913 tgctggctgggctggtcctcttgtaccaccgccggggcaaggccctggaggagccagcca 972
          ||||||||||||||||||    |    ||:|||||||||||| |||||||||||||| ||
Db    899 TGCTGGCTGGGCTGGTC--TCTTGTACAMCGCCGGGGCAAGG-CCTGGAGGAGCCAG-CA 954

Qy    973 atgatatcaaggaggatgc 991
          ||||||||||||||||||
Db    955 ATGATATCAAGGAGGATGC 973


RESULT  13
AL576327/c
LOCUS         AL576327                978 bp     mRNA     linear    EST
16-FEB-2001
DEFINITION  AL576327 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI073YP08 3
            prime, mRNA sequence.
ACCESSION   AL576327
VERSION     AL576327.1  GI:12938362
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 978)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .978
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI073YP08"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer.  Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      219 a    248 c    297 g    204 t     10 others
ORIGIN


  Query Match             49.4%;  Score 896;  DB 9;  Length 978;
  Best Local Similarity   97.1%;  Pred. No. 1.8e-201;
  Matches  943;  Conservative    9;  Mismatches   15;  Indels    4;  Gaps
4;

Qy    799 aggcccacaatgaggtgggcactgcccaatgtaatgtgacgctggaagtgagcacagggc 858
          | |||||||||||||| ||||||||||||:||||||||||||||||||||||||||||||
Db    977 AAGCCCACAATGAGGT-GGCACTGCCCAATKTAATGTGACGCTGGAAGTGAGCACAGGGC 919

Qy    859 ctggagctgcagtggttgctggagctgttgtgggtaccctggttggactggggttgctgg 918
          |||||||||||||||| |||||||||||||| |||||||||||||||||||||| ||||||
Db    918 CTGGAGCTGCAGTGGTAGCTGGAGCTGTTGT-GGTACCCTGGTTGGACTGGGGGTGCTGG 860

Qy    919 ctgggctggtcctcttgtaccaccgccggggcaaggccctggaggagccagccaatgata 978
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 CTGGGCTGGTCCTCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATA 800

Qy    979 tcaaggaggatgccattgctc-cccggaccctgccctggcccaagagctcagacacaatc 1037
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    799 TCAAGGAGGATGCCATTGCTCTCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATC 740

Qy   1038 tccaagaatgggacccttttcctctgtcacctccgcacgagccctccggccaccccatggc 1097
          |||||||:|    :| ||||:||||||||||||||||||||||||||||||||||||||
Db    739 TCCAAGAWTTTTTYCTTTTCYTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCCATGGC 680

Qy   1098 cctcccaggcctggtgcattgaccccacgcccagtctctccagccaggccctgccctca 1157
          |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 CCTCCCAGGCYTGGTGCATTGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCA 620

Qy   1158 ccaagactgcccacgacagatggggcccaccctcaaccaatatcccccatccctggtggg 1217
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    619 CCAAGACTGCCCACGACAGAT-GGGCCCACCCTCAACCAATATCCCCCATCCCTGGTGGG 561

Qy   1218 gtttcttcctctggcttgagccgcatgggtgctgtgcctgtgatggtgcctgcccagagt 1277
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    560 GTTTCTTCCTCTGGCTTGAGCCGCATGGGTGCTGTGCCTTTGATGGTGCCTGCCCAGAGT 501

Qy   1278 caagctggctctctggtatgatgaccccaccactcattggctaaaggatttggggtctct 1337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    500 CAAGCTGGCTCTCTGGTATGATGACCCCACCACTCATTGGCTAAAGGATTTGGGGTCTCT 441

Qy   1338 ccttcctataagggtcacctctagcacagaggcctgagtcatgggaaagagtcacactcc 1397
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    440 CCTTCCTATAGGGGTCACCTCTAGCACAGAGGCCTGAGTCATGGGAAAGAGTCACACTCC 381

Qy   1398 tgacccttagtactctgcccccacctctctttactgtgggaaaaccatctcagtaagacc 1457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    380 TGACCCTTAGTACTCTGCCCCCACCTCTCTTTACTGTGGGAAAACCATCTCAGTAAGACC 321

Qy   1458 taagtgtccaggagacagaaggagaagaggaagtggatctggaattgggaggagcctcca 1517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db    320 TAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGGAATTGGGAGGAGCCKCCA 261

Qy   1518 cccacccctgactcctccttatgaagccagctgctgaaattagctactcaccaagagtga 1577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    260 CCCACCCCTGACTCCTCCTTATGAAGCCAGCTGCTGAAATTAGCTACTCACCAAGAGTGA 201

Qy   1578 ggggcagagacttccagtcactgagtctcccaggcccccttgatctgtaccccacccctа 1637
          ||||||||||||:|||||||||||||||:||||||||||:||||||||||||||||||||
Db    200 GGGGCAGAGACTKCCAGTCACTGAGTCTSCCAGGCCCCCKTGATCTGTACCCCACCCCTA 141

Qy   1638 tctaacaccacccttggctcccactccagctccctgtattgatataacctgtcaggctgg 1697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    140 TCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGG 81
```

```
Qy   1698 cttggttaggttttactggggcagaggatagggaatctcttattaaaactaacatgaaat 1757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     80 CTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTCTTATTAAAACTAACATGAANT 21

Qy   1758 atgtgttgttt 1768
          || |  ||| |
Db     20 ATTTTGTGTAT 10


RESULT  14
AL546335
LOCUS       AL546335                938 bp     mRNA     linear    EST
16-FEB-2001
DEFINITION  AL546335 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI031YI09 5
            prime, mRNA sequence.
ACCESSION   AL546335
VERSION     AL546335.1  GI:12879351
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 938)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .938
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI031YI09"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer.  Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      168 a    282 c    281 g    205 t      2 others
ORIGIN


  Query Match             49.4%;  Score 895.8;  DB 9;  Length 938;
  Best Local Similarity   99.0%;  Pred. No. 2e-201;
  Matches  930;  Conservative    2;  Mismatches    4;  Indels    3;  Gaps
3;

Qy     10 ctgggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcctcggcacctg 69
          |||||||||||||||||||||||||||||||||||||||||||||||||||| :||||||||||
```

```
Db      1 CTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCA-SCTCGGCACCTG 59

Qy     70 caggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccagggagggccatga 129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 CAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGCCATGA 119

Qy    130 tttccctcccggggcccctggtgaccaacttgctgcggtttttgttcctggggctgagtg 189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 TTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGAGTG 179

Qy    190 ccctcgcgccccccctcgcgggcccagctgcaactgcacttgcccgccaaccggttgcagg 249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 CCCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGG 239

Qy    250 cggtggagggaggggaagtggtgcttccagcgtggtacaccttgcacggggaggtgtctt 309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 CGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTGTCTT 299

Qy    310 catcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaagaaaaggagg 369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 CATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGG 359

Qy    370 atcaggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtatccttggtct 429
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 ATCAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCT 419

Qy    430 actccatgccctcccggaacctgtccctgcggctggagggtctccaggagaaagactctg 489
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 ACTCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTG 479

Qy    490 gcccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggggccacagca 549
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 GCCCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCA 539

Qy    550 tcaaaaccttagaactcaatgtactggttcctccagctcctccatcctgccgtctccagg 609
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 TCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGG 599

Qy    610 gtgtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaaggagtaagcccg 669
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 GTGTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCG 659

Qy    670 ctgtccaataccagtgggatcggcagcttccatccttccagactttctttgcaccagcat 729
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 CTGTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCAT 719

Qy    730 tagatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatggctggagtct 789
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 TAGATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCT 779

Qy    790 atgtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgctggaagtga 849
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 ATGTCTGCAAGGCCCACAATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGA 839

Qy    850 gcacagggcctggagctgcagtggttgctggagctgttgtgggtaccctggttggactgg 909
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    840 GCACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTA-CCTGGTTGGACTGG 898
```

```
Qy    910 ggttgctggctgggctggtcctcttgtaccaccgccggg 948
          |||||||||||||||||| ||||||||| ||  | ||:
Db    899 GGTTGCTGGCTGGGCTGGT-CTCTTGTACAACGCCGGGS 936


RESULT  15
AL554790
LOCUS       AL554790                999 bp     mRNA     linear    EST
16-FEB-2001
DEFINITION  AL554790 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI086YJ14 5
            prime, mRNA sequence.
ACCESSION   AL554790
VERSION     AL554790.1  GI:12895912
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 999)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .999
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI086YJ14"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer.  Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      184 a    298 c    302 g    214 t      1 others
ORIGIN

  Query Match             49.4%;  Score 895.8;  DB 9;  Length 999;
  Best Local Similarity   98.8%;  Pred. No. 2.1e-201;
  Matches  934;  Conservative    0;  Mismatches    7;  Indels    4;  Gaps
3;

Qy     12 gggtgtcagcggctcggctcccgcgcacgctccggccgtcgcgcagcctcggcacctgca 71
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db      1 GGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCA-CCTCGGCACCTGCA 59

Qy     72 ggtccgtgcgtcccgcggctggcgcccctgactccgtcccggccagggagggccatgatt 131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 GGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGCCATGATT 119

Qy    132 tccctcccggggcccctggtgaccaacttgctgcggtttttgttcctggggctgagtgcc 191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 TCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGAGTGCC 179

Qy    192 ctcgcgccccctcgcgggcccagctgcaactgcacttgcccgccaaccggttgcaggcg 251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 CTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAGGCG 239

Qy    252 gtggagggaggggaagtggtgcttccagcgtggtacaccttgcacggggaggtgtcttca 311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 GTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTGTCTTCA 299

Qy    312 tcccagccatgggaggtgccctttgtgatgtggttcttcaaacagaaagaaaaggaggat 371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 TCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGAT 359

Qy    372 caggtgttgtcctacatcaatggggtcacaacaagcaaacctggagtatccttggtctac 431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 CAGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTAC 419

Qy    432 tccatgccctcccggaacctgtccctgcggctggagggtctccaggagaaagactctggc 491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 TCCATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGC 479

Qy    492 ccctacagctgctccgtgaatgtgcaagacaaacaaggcaaatctaggggccacagcatc 551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 CCCTACAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATC 539

Qy    552 aaaaccttagaactcaatgtactggttcctccagctcctccatcctgccgtctccagggt 611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 AAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGT 599

Qy    612 gtgccccatgtgggggcaaacgtgaccctgagctgccagtctccaaggagtaagcccgct 671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 GTGCCCCATGTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCT 659

Qy    672 gtccaataccagtgggatcggcagcttccatccttccagactttctttgcaccagcatta 731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 GTCCAATACCAGTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTA 719

Qy    732 gatgtcatccgtgggtctttaagcctcaccaacctttcgtcttccatggctggagtctat 791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    720 GATGTCATCCGTGGGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTAT 779

Qy    792 gtctgcaaggcccacaatgaggtgggcactgcccaatgtaatgtgacgctggaagtgagc 851
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    780 GTCTGCAAGGCCCACAATGAGGTGGGCACTGCCAAATGTAATGTGACGCTGGAAGTGAGC 839

Qy    852 acagggcctggagctgcagtggttgctggagctgttgtgggtaccctggttggactgggg 911
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    840 ACAGGGCCTGGAGCTGCAGTGGTTGCTGGAGCTGTTGTGGGTA-CCTGGTTGGACTGGGG 898

Qy    912 ttgctggctgggctggtcctcttgtaccaccgccggggcaaggcc 956
          |||||||||||||||||    |    ||||||||||||||||||
Db    899 TTGCTGGCTGGGCTGGTC--TCTTGTACACCGCCGGGGCAAGGCC 941

Search completed: August 19, 2002, 15:31:47
Job time: 1850 sec
```

ALIGNMENTS

RESULT 1
CXAR_MOUSE
ID CXAR_MOUSE STANDARD; PRT; 365 AA.
AC P97792; O09052;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Coxsackievirus and adenovirus receptor homolog precursor (mCAR).
GN CXADR OR CAR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=97190109; PubMed=9036860;
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT "Isolation of a common receptor for Coxsackie B viruses and
RT adenoviruses 2 and 5.";
RL Science 275:1320-1323(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/MAI;
RX MEDLINE=97250541; PubMed=9096397;
RA Tomko R.P., Xu R., Philipson L.;
RT "HCAR and MCAR: the human and mouse cellular receptors for subgroup C
RT adenoviruses and group B coxsackieviruses.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA Bergelson J.M., Krithivas A., Crowell T.L., Finberg R.W.;
RT "The murine CAR homologue (mCAR) is a receptor for coxsackie B
RT viruses and adenoviruses.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; Y10320; CAA71368.1; -.
DR EMBL; U90715; AAC53148.1; -.
DR EMBL; Y11929; CAA72679.1; -.
DR MGD; MGI:1201679; Cxadr.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00410; IG_like; 1.

```
DR   SMART; SM00408; IGc2; 1.
KW   Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Repeat.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    365       COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR
FT                                 HOMOLOG.
FT   DOMAIN       20    237       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    238    258       POTENTIAL.
FT   DOMAIN      259    365       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       34    127       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN      155    219       IG-LIKE C2-TYPE DOMAIN 2.
FT   DISULFID     41    120       BY SIMILARITY.
FT   DISULFID    162    212       BY SIMILARITY.
FT   CARBOHYD    106    106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    201    201       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    340    365       VAAPNLSRMGAVPVMIPAQSKDGSIV -> FKYAYKTDGIT
FT                                 VV (IN REF. 2 AND 3).
SQ   SEQUENCE   365 AA;  39947 MW;  5445B4B52A34B2A2 CRC64;


  Query Match             17.6%;  Score 353.5;  DB 1;  Length 365;
  Best Local Similarity   27.8%;  Pred. No. 1.8e-16;
  Matches  113;  Conservative   71;  Mismatches  156;  Indels   67;  Gaps   15;

Qy       9 VTNLLRFLFL-GLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSSSQPWE 67
Db       1 MARLLCFVLLCGIADFT----SGLSITTPEQRIEKAKGETAYLPCKFTLSPE--DQGPLD 54

Qy      68 VPFVMWFFKQKEKE--DQVLSYINGVTTSKPGVSLVY----------------SMPSRNL 109
Db      55 IE---WLISPSDNQIVDQVIILYSG--------DKIYDNYYPDLKGRVHFTSNDVKSGDA 103

Qy     110 SLRLEGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGAN 169
Db     104 SINVTNLQLSDIGTYQCKVK------KAPGVANKKFLLTVLVKPSGTRCFVDGSEEIGND 157

Qy     170 VTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPAL-DVIRGSLSLTNLSSSMAGVYVCKAHN 228
Db     158 FKLKCEPKEGSLPLQFEW-QKLSDSQTMPTPWLAEMTSPVISVKNASSEYSGTYSCTVQN 216

Qy     229 EVGTAQCNVTLE-VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRR---GKALEEPAND 284
Db     217 RVGSDQCMLRLDVVPPSNRAGTIAGAVIGTLLALVLIGAILFCCHRKRREEKYEKEVHHD 276

Qy     285 IKEDAIAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPS 344
Db     277 IRED------VPPPKSRTSTARSYIGSNHSSL-----------GSMSPSNMEGYSKTQY 318

Qy     345 PRLPTTDGAH-PQPISPIPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390
Db     319 NQVPSEDFERAPQSPTLAPAKVAAPNLSRMGAVPVMIPAQSKDGSIV 365
```

```
RESULT   2
CXAR_HUMAN
ID   CXAR_HUMAN     STANDARD;      PRT;   365 AA.
AC   P78310; O00694;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Coxsackievirus and adenovirus receptor precursor (Coxsackievirus B-
DE   adenovirus receptor) (hCAR) (CVB3 binding protein).
GN   CXADR OR CAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97190109; PubMed=9036860;
RA   Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA   Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT   "Isolation of a common receptor for Coxsackie B viruses and
RT   adenoviruses 2 and 5.";
RL   Science 275:1320-1323(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97250541; PubMed=9096397;
RA   Tomko R.P., Xu R., Philipson L.;
RT   "HCAR and MCAR: the human and mouse cellular receptors for subgroup C
RT   adenoviruses and group B coxsackieviruses.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20008750; PubMed=10543405;
RA   Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,
RA   Bowles N.E.;
RT   "Genomic organization and chromosomal localization of the human
RT   Coxsackievirus B-adenovirus receptor gene.";
RL   Hum. Genet. 105:354-359(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;
RT   "Sequence and expression of CXADR, the human gene for the
RT   coxsackievirus and adenovirus receptor.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND
CC       SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC   -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y07593; CAA68868.1; -.
DR   EMBL; U90716; AAC51234.1; -.
DR   EMBL; AF169366; AAF05908.1; -.
DR   EMBL; AF169360; AAF05908.1; JOINED.
```

```
DR   EMBL; AF169361; AAF05908.1; JOINED.
DR   EMBL; AF169362; AAF05908.1; JOINED.
DR   EMBL; AF169363; AAF05908.1; JOINED.
DR   EMBL; AF169364; AAF05908.1; JOINED.
DR   EMBL; AF169365; AAF05908.1; JOINED.
DR   EMBL; AF200465; AAF24344.1; -.
DR   MIM; 602621; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00410; IG_like; 1.
DR   SMART; SM00408; IGc2; 1.
KW   Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Repeat.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    365       COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.
FT   DOMAIN       20    237       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    238    258       POTENTIAL.
FT   DOMAIN      259    365       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       34    127       IG-LIKE C2-TYPE DOMAIN 1.
FT   DOMAIN      155    219       IG-LIKE C2-TYPE DOMAIN 2.
FT   DISULFID     41    120       BY SIMILARITY.
FT   DISULFID    162    212       BY SIMILARITY.
FT   CARBOHYD    106    106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    201    201       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   365 AA;  40029 MW;  AB01C6346CB7FE64 CRC64;


  Query Match             17.0%;  Score 343;  DB 1;  Length 365;
  Best Local Similarity   27.5%;  Pred. No. 9e-16;
  Matches  106;  Conservative   67;  Mismatches  147;  Indels   66;  Gaps   14;

Qy      31 LQLHLPANRLQAVEGGEVVLPAWYTLHGEVSSSQPWEVPFVMWFFK--QKEKEDQVLSYI 88
           | :  |   ::  :|    ||  :||  |     | ::    |       :| |||:
Db      20 LSITTPEEMIEKAKGETAYLPCKFTLSPE--DQGPLDIE---WLISPADNQKVDQVIILY 74

Qy      89 NGVTTSKPGVSLVY---------------SMPSRNLSLRLEGLQEKDSGPYSCSVNVQD 132
           :|          :|                   : | : |: :  ||  | | | | |
Db      75 SG--------DKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVK--- 123

Qy     133 KQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLP 192
              |: | : | : | ||| |:   | : |   :|::  : |:       :||:| :
Db     124 ---KAPGVANKKIHLVVLVKPSGARCYVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSD 180

Qy     193 SFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE-VSTGPGAAVVA 251
           | :   :   ::    :|: | ||  :| | |   | ||: || : |  |      | ::|
Db     181 SQKMPTSWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSDQCLLRLNVVPPSNKAGLIA 240

Qy     252 GAVVGTLVGLGLLAGLVLLYHRRGKALE----EPANDIKEDAIAPRTLPWPKSSDTISKN 307
           ||::|||: | |: ||::   |: :  |    |  :||:||      :| |||  : :::
Db     241 GAIIGTLLALALI-GLIIFCCRKKRREEKYEKEVHHDIRED------VPPPKSRTSTARS 293

Qy     308 GTLSSVTSARALRPPH--GPPRPGALTPTPSLSSQALP-SPRLPTTDGAHPQPISPIPGG 364
              |: :|  :: | :  |  :        ||   :  | || ||             |
Db     294 YIGSNHSSLGSMSPSNMEGYSKT-QYNQVPSEDFERTPQSPTLP------------PAK 339

Qy     365 VSSSGLSRMGAVPVMVPAQSQAGSLV 390
           |::  ||||||:|||:||||: ||:|
Db     340 VAAPNLSRMGAIPVMIPAQSKDGSIV 365
```